

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 5, 2004, 16:29:20 ; Search time 54 Seconds
(without alignments)
83.718 Million cell updates/sec

Title: US-09-591-789-1

Perfect score: 96

Sequence: 1 CKPISGHNSLFWYRQT 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: 1: Geneseq_29Jan04:*

1: geneseqp1808:.*
2: geneseqp1908:.*
3: geneseqp2008:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	16	AAV17984	Aay17984 Peptide d
2	96	100.0	16	AAE17904	Aae17904 T-cell re
3	96	100.0	16	ABB82940	Abb82940 T-cell re
4	96	100.0	14	AAU97093	Aau97093 T-cell re
5	96	100.0	312	1 AAP50079	Aap50079 T-cell an
6	96	100.0	312	1 AAP60471	Aap60471 Portion o
7	85	88.5	114	5 AAU97094	Aau97094 T-cell re
8	82	85.4	312	2 AAES3145	Aae33145 T-cell an
9	80	83.3	114	2 AAR26960	Aar26960 Human T 1
10	74	77.1	79	2 AAR26969	Aar26969 Human T 1
11	74	77.1	92	2 AAR65454	Aar65454 T-cell re
12	74	77.1	93	2 AAY23521	Aay23521 Amino aci
13	74	77.1	94	2 AAR78686	Aar78686 T-cell re
14	74	77.1	96	2 AAR78687	Aar78687 T-cell re
15	74	77.1	104	2 AAR65453	Aar65453 T-cell re
16	74	77.1	106	2 AAY23520	Aay23520 Amino aci
17	74	77.1	113	2 AAR65450	Aar65450 T-cell re
18	74	77.1	113	2 AAR65455	Aar65455 T-cell re
19	74	77.1	114	2 AAY23517	Aay23517 Amino aci
20	74	77.1	114	2 AAY23522	Aay23522 Amino aci
21	74	77.1	184	4 AA012565	Aa012565 Human pol
22	74	77.1	311	3 AAY96291	Aay96291 Human IGF
23	74	77.1	311	5 AAU76920	Aau76920 Human T c
24	74	77.1	314	4 AAW99374	Aaw99374 Human T-c
25	74	77.1	324	4 AAU30870	Aau30870 Novel hum

ALIGNMENTS

26	73	76.0	113	2	AAR65452	Aar65452 T-cell re
27	73	76.0	114	2	AAR26968	Aar26968 Human T 1
28	73	76.0	114	2	AAY23519	Aay23519 Amino aci
29	72	75.0	113	2	AAR65451	Aar65451 T-cell re
30	72	75.0	114	2	AAY23518	Aay23518 Amino aci
31	72	75.0	314	2	AAY15229	Aay15229 Human rec
32	70	72.9	79	2	AAR26964	Aar26964 Human T 1
33	70	72.9	114	2	AAR65467	Aar65467 T-cell re
34	70	72.9	114	2	AAY23534	Aay23534 Amino aci
35	70	72.9	137	2	AAW25939	Aaw25939 T-cell re
36	70	72.9	287	3	AAV56079	Aav56079 Mouse H2-
37	70	72.9	287	3	AAV56081	Aav56081 HLA-A2/HL
38	70	72.9	287	3	AAV57857	Aav57857 TCR beta
39	70	72.9	287	3	AAV57855	Aav57855 TCR beta
40	69	71.9	113	2	AAR65456	Aar65456 T-cell re
41	69	71.9	114	2	AAY23523	Aay23523 Amino aci
42	68	70.8	312	3	AAY69988	Aay69988 Human rec
43	65	67.7	92	2	AAR79171	Aar79171 TCR Vbeta
44	63	65.6	244	7	ADC75006	Adc75006 Soluble A
45	63	65.6	345	3	AAY69986	Aay69986 Human rec

RESULT 1
AAV17984
ID AAY17984 standard; peptide: 16 AA.

AAV17984;
09-AUG-1999 (first entry)

Peptide derived from human T-cell receptor Vbeta gene product.

XX T-cell receptor; TCR; immunodeficiency type retrovirus; immune response;
XX cytokine; C-type retrovirus; lentivirus; T helper 1; Th1; interleukin;
XX interferon-gamma; Th2; immunoglobulin G; AIDS; immune deficiency;
XX immunosuppression; cytokine dysregulation; TCR Vbeta gene.

OS Homo sapiens.

PN US5911990-A.

XX 15-JUN-1999.

PF 13-AUG-1996; 96US-00696049.

XX 13-AUG-1996; 96US-00696049.

PR (ARIZ-) ARIZONA BOARD OF REGENTS.

XX Wang Y, Huang DS, Watson RR, Marchalonis JJ, Dehghanipishneh K;

PS WPI: 1999-357172/30.

XX Delaying onset of AIDS in a host infected with an immunodeficiency-type
PT retrovirus.

XX Claim 3; Col 9; 13pp; English.

The invention relates to a peptide (I) corresponding to the first complementarity determining region of T-cell receptor V beta 1. Administering this peptide to a host infected with an immunodeficiency type retrovirus results in the prevention of retrovirus-induced suppression of immune responses and normalizes cytokine production. The invention describes (1) a method of modulating the immune response of a mammal infected with a C-type retrovirus or a lentivirus by administering the TCR peptide through a systemic route to stimulate production of T helper 1 (Th1) cytokines; interleukin 2 and interferon-gamma, and to suppress the production of T helper 2 (Th2); interleukins 5, 6 and 10 and immunoglobulin G; and (2) a method of altering the immune system response of a host suffering from an infectious disease by artificially

introducing the peptide by injection into the host's bloodstream or immune system so that the immune system is artificially induced to stimulate production of Th1 cytokines or suppress production of Th2 derived cytokines. Administration of the peptide is used to delay the onset of AIDS through the restoration of normal levels of Th1 cytokines and Th2 derived cytokines and extends the period that occurs between infection by the retrovirus and the appearance of immune deficiencies. It causes the deleterious effects of infection to be reversed through prevention of immunosuppression and cytokine dysregulation that is otherwise induced by infection with an immunodeficiency-type retrovirus. The present sequence represents the peptide of the invention derived from TCR Vbeta gene product

Sequence 16 AA;

Query Match 100.0%; Score 96; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGHNSLFWYRQT 16
DB 1 CKPISGHNSLFWYRQT 16

RESULT 2
AAE17904
ID AAE17904 standard; peptide; 16 AA.
XX
AC AAE17904;
XX
DT 07-MAY-2002 (first entry)
XX
DE T-cell receptor-derived peptide #1.
XX
KM T-cell receptor; TCR-derived peptide; cardiovascular disorder; AIDS; acquired immune deficiency syndrome; HIV; human immunodeficiency virus; Th1 cytokine; atherosclerosis; arteriosclerosis; reperfusion injury; atherosclerotic heart disease; myocardial infarction; cardiac arrest; thrombus formation; allergy; asthma; septic shock; anaphylactic shock; delayed hypersensitivity; tumour; sarcoma; carcinoma; lymphoma; cancer; astrocytoma; glioma; melanoma; cardiac; vasotropic; immunosuppressive; cytostatic; antibacterial; virucide; fungicide.
XX
OS Unidentified.
XX
PN WO200195785-A2.
XX
PD 20-DEC-2001.
XX
PF 12-JUN-2001; 2001WO-US018817.
XX
PR 12-JUN-2000; 2000US-00591789.
XX
PA (ARIZ-) ARIZONA BOARD OF REGENTS.
XX
PI Marchalonis JJ, Watson RR, Schluter SF;
XX
DR WPI; 2002-139689/18.
XX
PT New T-cell receptor-derived peptides for preventing and/or treating human immunodeficiency virus infection, cardiovascular diseases and disorders and allergic disease.
XX
PS Claim 4; Page 25; 37pp; English.
XX
CC The patent discloses T-cell receptor (TCR)-derived peptides or their derivatives. The invention also relates to methods for the prevention and/or treatment of cardiovascular and allergic diseases and disorders, methods for inhibiting the growth of or reducing the volume of a solid tumour and methods for preventing the progression to acquired immune deficiency syndrome (AIDS) in a HIV (human immunodeficiency virus) positive human. The method involves administration of TCR derived peptides. Peptides of the invention are useful for increasing the

production of Th1 cytokines (e.g., interleukin (IL)-2, interferon- gamma or to decrease production of Th2 cytokines (e.g., IL-4, IL-5, IL-6, IL-10 or immunoglobulin G (IgG)) in an individual free of infection with an immunodeficiency-type retrovirus. They are useful for reversing the deleterious effects of infection with an immunodeficiency-type retrovirus (HIV), preventing or treating a disease or disorder of the cardiovascular system (e.g., atherosclerosis, atherosclerotic heart disease, arteriosclerosis, reperfusion injury, myocardial infarction, cardiac arrest, thrombus formation and retrovirus-induced cardiovascular dysfunction and allergic diseases or disorders characterised by increased immunoglobulin E (IgE) production (e.g., allergy, asthma, septic shock, anaphylactic shock and delayed hypersensitivity). TCR-derived peptides are also useful for inhibiting the growth of a solid tumour or reducing the volume of a solid tumour such as sarcomas, carcinomas, lymphomas and other solid tumour cancers, tumours of the germ line, central nervous system, prostate, breast, cervical, uterine, lung, ovarian, testicular, thyroid, stomach, pancreatic, liver or colon cancer tumour, astrocytoma, glioma or melanoma tumour. They are useful for preventing immunosuppression or suppressing progression to immune dysfunction or cytokine dysregulation in an individual infected with a viral, fungal or bacterial infectious agent other than an immunodeficiency-type retrovirus. The present sequence is a TCR-derived peptide of the invention

Sequence 16 AA;

Query Match 100.0%; Score 96; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGHNSLFWYRQT 16
DB 1 CKPISGHNSLFWYRQT 16

RESULT 3
ABB82940
ID ABB82940 standard; peptide; 16 AA.
XX
AC ABB82940;
XX
DT 14-APR-2003 (first entry)
XX
DE T-cell receptor beta chain clone Y735 beta3 peptide.
XX
KM TCR; beta3 peptide; T-cell receptor; virucide; antibacterial; interferon; protozoacide; fungicide; anti-HIV; immunosuppressive; cytostatic; Vbeta; tuberculostatic; antiallergic; cardiac; antiarthritic; antineumatic; antiarteriosclerotic; antithyroid; antidiabetic; dermatological; vaccine; cardiovascular; nootropic; neuroleptic; cytokine; interleukin.
XX
OS Homo sapiens.
XX
PN WO200294860-A2.
XX
PD 28-NOV-2002.
XX
PF 17-MAY-2002; 2002WO-GB002323.
XX
PR 18-MAY-2001; 2001GB-00012126.
XX
PA (ARIZ-) ARIZONA BOARD OF REGENTS.
XX
PI (BASS/) BASSETT R S.
XX
DR Marchalonis JJ, Watson RR;
XX
PS WPI; 2003-140358/13.
XX
CC New homodimer comprising peptides from a T-cell receptor, useful for manufacturing a medicament for modulating or altering an immune response, stimulating the production of Th1 cytokines or suppressing production of Th2 cytokines.

PS Claim 1; Page 35; 49pp; English.

XX
CC The invention relates to a homodimer where each monomer of the homodimer
CC consists of Sequence A (AB882940), from the N-terminus to the C-terminus
CC direction, where if the sequences are present as an aqueous solution,
CC then 81 % of the occurrences of the sequence are present as a dimer. Each
CC monomer of the homodimer is a homologue of the beta2 peptide of the T-
CC cell receptor beta chain clone YR35, where the beta2 peptide consists of
CC Sequence A, and the homologue has the sequence of a segment of another
CC distinct human Vbeta gene that corresponds to the same segment as the
CC beta2 peptide. The new dimer is useful in the manufacture of a medicament
CC for modulating or altering the immune response of an animal, or for
CC stimulating the production of Th1 cytokines and/or suppressing production
CC of Th2 cytokines and/or improving general immune competence. It is also
CC useful for treating a condition in which auto-antibodies against the
CC family of T-cell receptor (TCR) Vbeta CDR (complementarily determining
CC regions) peptides are generated, or for preventing or reversing
CC immunosuppression and/or abnormal cytokine production. The medicament is
CC additionally used for treating an infectious disease, preferably caused
CC by a virus, or for preventing or reversing the deleterious effects of an
CC immunodeficiency-type retrovirus, where the infectious disease is caused
CC by a C-type retrovirus or a lentivirus. The lentivirus is human
CC immunodeficiency virus (HIV)-1, HIV-2, HIV-3, simian immunodeficiency
CC virus (SIV) or feline immunodeficiency virus (FIV), and where the
CC lentivirus is HIV, the medicament is for preventing the onset of AIDS.
CC The infectious disease is also a non-viral pathogen such as protozoal,
CC bacterial or fungal infection, and is caused by a species of Leishmania,
CC leprosy, Cryptosporidium, Coccidioides immitis, listeria, coccidiomycosis
CC or mycobacterium, preferably tuberculosis. The medicament is also used
CC for treating an autoimmune disease, preferably lupus, or for treating an
CC allergic disease such as allergic rhinitis or atopic dermatitis, or for
CC treating cancer patients immunocompromised because of chemotherapy. It
CC can also be used for treating cardiac patients, where the cardiac patient
CC has been infected by a virus which causes inflammatory heart disease. The
CC medicament is preferably a vaccine, where the dimers serve as an
CC adjuvant, and the vaccine is a flu vaccine. The auto-antibodies against
CC the family of TCR Vbeta CDR peptides are generated as a result of contact
CC between the animal and an oil or adjuvant. The medicament is additionally
CC used for treating immune dysfunction and abnormal cytokine production
CC induced by the aging process. The TCR Vbeta CDR1 peptide or its variant
CC is useful in the treatment or prevention of a viral or non-viral
CC pathogenic disease such as a protozoal infection (Leishmaniasis), a
CC bacterial or fungal infection (Coccidiomycosis), leprosy, an autoimmune
CC disease (rheumatoid arthritis, Crohn's disease, insulin-dependent
CC diabetes mellitus, multiple sclerosis, atherosclerosis, Hashimoto's
CC thyroiditis, celiac disease, myasthenia gravis, pemphigus vulgaris,
CC systemic lupus erythematosus (SLE), Grave's disease, systemic vasculitis,
CC reduction of immunocompetence due to contact to environmental agents for
CC example oils and adjuvants, an allergic disease (asthma, allergic
CC rhinitis or atopic dermatitis), cancer (lymphoid tumor, melanoma or
CC breast cancer), cardiac conditions, or as an adjuvant, for example in flu
CC or other vaccine. The present sequence represents the beta2 peptide of
CC the TCR beta chain clone YR35
XX

SQ Sequence 16 AA;

Query Match 100.0%; Score 96; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYRQT 16
| | | | | | | | | | | | | | | |
DB 1 CKPISGNSLFWYRQT 16

RESULT 4
AAU97093

ID AAU97093 standard; protein; 114 AA.

AC AAU97093;

XX 14-AUG-2002 (first entry)
XX

DE T cell receptor variable region Vbeta8.1.

XX T cell receptor variable region; beta2 glycoprotein I; beta2GPI;

KW anti-phospholipid; immunogenic; antimetabolite; receptor;

XX anti-phospholipid antibody syndrome; Vbeta8.1.

OS Homo sapiens.

XX JP2002112784-A.

XX 16-APR-2002.

PF 05-OCT-2000; 2000JP-00306677.

XX 05-OCT-2000; 2000JP-00306677.

PA (KEIO-) GH KEIO GIJUKU.

XX WPI; 2002-448756/48.

PT Variable region of T cell receptor for treating anti-phospholipid

PT antibody syndrome, and a single chain peptide inducing immunoreaction on

XX beta2 glycoprotein I-reactive T cell.

PS Disclosure; Fig 1; 18pp; Japanese.

XX The invention relates to variable region of T cell receptor for treating

CC anti-phospholipid antibody syndrome, and a single chain peptide inducing

CC immunoreaction on beta2 glycoprotein I (beta2GPI)-reactive T cell. The

CC peptide is used as a preventive and treating agent for anti-phospholipid

CC antibody syndrome. The present sequence represents the amino acid

XX sequence of a T cell receptor variable region Vbeta8.1

SQ Sequence 114 AA;

Query Match 100.0%; Score 96; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYRQT 16
| | | | | | | | | | | | | | | |
DB 42 CKPISGNSLFWYRQT 57

RESULT 5
AAP50079
ID AAP50079 standard; protein; 312 AA.

XX AAP50079;

XX 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 19-MAR-1992 (first entry)

XX T-cell antigen receptor protein.

XX T-cell receptor; DNA probe; tumor marker; ss.

XX Homo sapiens.

OS Mus sp.

XX EPI49548-A.

XX 24-JUL-1985.

XX 14-JAN-1985; 85EP-00300243.

XX 13-JAN-1984; 84US-00570694.

XX 06-FEB-1984; 84US-00577526.

XX (ONTA-) ONTARIO CANCER INST.

XX Mak TW;

XX WPI; 1985-179193/30.
 DR N-PSDB; AAN50091.
 XX
 PT New nucleic acid encoding T-cell antigen receptor polypeptide - useful
 PT for prepn. of probes or antibodies for detection of tumour cells and T-
 PT cells.
 XX
 PS Disclosure; Fig 3; 15pp; English.
 XX
 CC This protein resembles human and mouse Ig light chain molecules. This
 CC protein is encoded by clone Y135 and is part of the antigen receptor
 CC mediating specialized T-lymphocyte function. Antibodies may be directed
 CC against this protein and used for detection of T-cell receptor antigen so
 CC that unknown cells, e.g. a tumor cell, can be identified as a T-cell or
 CC other cell. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on
 CC 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 312 AA;

Query Match 100.0%; Score 96; DB 1; Length 312;
 Best Local Similarity 100.0%; Pred. No. 4.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYRQT 16
 DB 42 CKPISGNSLFWYRQT 57

RESULT 6
 ID AAP60471 standard; protein; 312 AA.
 AC AAP60471;

DT 13-JUN-1991 (first entry)
 DE Portion of a human T-cell antigen receptor protein.
 XX
 KM Cancer; tumour cell; T-cell receptor.

OS Homo sapiens.
 XX
 PN CA1197480-A.
 PD 03-DEC-1985.
 XX
 PF 01-FEB-1984; 84CA-00446545.
 XX
 PR 01-FEB-1984; 84CA-00446545.
 XX
 PA (ONTA-) ONTARIO CANCER INST.
 XX

PI Mak TW;
 XX
 DR WPI; 1986-007147/02.
 DR N-PSDB; AAN60406.
 XX

PT New pure nucleic acid with sequence encoding T-cell polypeptide - is
 PT prepd. by recombinant DNA methods for use as probe when labelled and for
 PT antibody prodn.
 PT

PS Claim 4; Fig 3; 22pp; English.

XX Receptor protein product has at least 60% homology with the clone Y135.
 CC The product resembles human and mouse Ig light chain molecules, and may
 CC be labelled for use as a probe for the detection of the T-cell receptor
 CC antigen, and identification of unknown (esp. tumour cells) as T-cells
 CC

SQ Sequence 312 AA;

Query Match 100.0%; Score 96; DB 1; Length 312;
 Best Local Similarity 100.0%; Pred. No. 4.2e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CKPISGNSLFWYRQT 16
 DB 42 CKPISGNSLFWYRQT 57

RESULT 7
 ID AAU97094 standard; protein; 114 AA.

AC AAU97094;
 DT 14-AUG-2002 (first entry)
 DE T cell receptor variable region Vbeta8.2.

XX T cell receptor variable region; beta2 glycoprotein I; beta2GPI;
 KM anti-phospholipid; immunogenic; antimecabolite; receptor;
 KM anti-phospholipid antibody syndrome; Vbeta8.2.

OS Homo sapiens.

PN JP2002112784-A.

PD 16-APR-2002.

PF 05-OCT-2000; 2000JP-00306677.

PR 05-OCT-2000; 2000JP-00306677.

PA (KEIO-) GH KEIO GIUTKU.

DR WPI; 2002-448756/48.

PT Variable region of T cell receptor for treating anti-phospholipid
 PT antibody syndrome, and a single chain peptide inducing immunoreaction on
 PT beta2 glycoprotein I-reactive T cell.
 XX

PS Disclosure; Fig 1; 18pp; Japanese.

CC The invention relates to variable region of T cell receptor for treating
 CC anti-phospholipid antibody syndrome, and a single chain peptide inducing
 CC immunoreaction on beta2 glycoprotein I (beta2GPI)-reactive T cell. The
 CC peptide is used as a preventive and treating agent for anti-phospholipid
 CC antibody syndrome. The present sequence represents the amino acid
 CC sequence of a T cell receptor variable region Vbeta8.2
 CC

SQ Sequence 114 AA;

Query Match 88.5%; Score 85; DB 5; Length 114;
 Best Local Similarity 87.5%; Pred. No. 8.5e-06;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYRQT 16
 DB 42 CKPISGNSLFWYRQT 57

RESULT 8
 ID AAR53145 standard; protein; 312 AA.

AC AAR53145;

DT 25-MAR-2003 (revised)

DR 08-SEP-1994 (first entry)

DE T-cell antigen receptor.

XX T-cell antigen receptor; T-lymphocyte; probe; hybridization; MOLT-3.

OS Homo sapiens.

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XX Key Location/Qualifiers
FH Misc-difference 90 /note= "possible N-glycosylation site"
FT Misc-difference 205 /note= "possible N-glycosylation site"
FT
XX EP593092-A1.
XX
XX 20-APR-1994.
XX
XX 14-JAN-1985; 93BP-00118895.
XX
XX 13-JAN-1984; 84US-00570694.
XX 06-FEB-1984; 84US-00577526.
XX 14-JAN-1985; 85EP-00300243.
XX
XX (OMTA-) ONTARIO CANCER INST.
XX
XX Mak TW;
XX
XX WPI; 1994-127936/16.
XX N-PSDB; AAQ62128.
XX
XX New nucleic acid encoding T-cell antigen receptor - is useful e.g. as a
XX probe to identify T-cells.
XX
XX Disclosure; Fig 3; 13pp; English.
XX
XX mRNA complementary to the DNA sequence given in AAQ62128 is obtained by
XX isolating mRNA from MOLT-3 cells, preparing cDNA, inserting the cDNA into
XX the BglII site of vector pPP502B5, transfecting the vector into
XX Escherichia coli HB101, and screening for 1.3 kb T-cell specific mRNA in
XX MOLT-3 and HSC-56 cells. The mRNA encodes a portion of the T-cell antigen
XX receptor (sequence AAR3145). (Updated on 25-MAR-2003 to correct PN
XX field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-
XX 2003 to correct PR field.)
XX
XX Sequence 312 AA;
XX
XX Query Match 85.4%; Score 82; DB 2; Length 312;
XX Best Local Similarity 93.8%; Pred. No. 7.4e-05;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 CKPISGNSLFMYROT 16
XX |||||
XX 42 CKPISGNSLFMYROT 57
XX
XX RESULT 9
XX AAR26960
XX ID AAR26960 standard; protein; 114 AA.
XX
XX AAR26960;
XX
XX 25-MAR-2003 (revised)
XX 11-FEB-1993 (first entry)
XX
XX Human T lymphocyte receptor V-beta w21 subfamily segment.
XX
XX TCR; IGR b 02; variable region; immunomodulation;
XX polymerase chain reaction; T cell receptor.
XX
XX Homo sapiens.
XX
XX WO9213950-A2.
XX
XX 20-AUG-1992.
XX
XX 12-FEB-1992; 92WO-FR000130.
XX
XX 12-FEB-1991; 91FR-00001613.
XX 12-APR-1991; 91FR-00004523.
XX
XX

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XX
XX (ROUS ) ROUSSEL-UCIAF.
XX
XX Hercend T, Triebel F, Roman-Roman S, Ferradini L;
XX
XX WPI; 1992-300036/36.
XX N-PSDB; AAQ28173.
XX
XX Variable regions of b-chain of T-lymphocyte receptors and their DNA -
XX useful as immuno:modulant(s) and for diagnosing immune disorders.
XX
XX Claim 7; Page 37; 75pp; French.
XX
XX RNA was isolated from peripheral lymphocytes and converted to cDNA using
XX a C-beta-specific primer. The cDNA was amplified by anchored PCR using C-
XX beta and polyC primers, then amplified again using a different C-beta
XX specific primer. The amplified product was SacII-restricted, inserted
XX into Bluescript SK+ vector and used to transform E.coli XL-1blue.
XX Transformants were screened with a C-beta specific probe and DNA from
XX positive clones was sequenced in the C-beta region. The sequence
XX designated "IGR b 02" has ca. 85% homology with the sequence HSTCRB23
XX (see Wilson R.K. et al., Immunogenetics 32:406, 1990) and is a member of
XX the Vbeta w21 subfamily. The peptide encoded by it can be used to block T
XX cell epitopes and in vaccines. See also AAQ28174-Q28228. (Updated on 25-
XX MAR-2003 to correct PN field.)
XX
XX Sequence 114 AA;
XX
XX Query Match 83.3%; Score 80; DB 2; Length 114;
XX Best Local Similarity 80.0%; Pred. No. 5.4e-05;
XX Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 CKPISGNSLFMYROT 15
XX |||||
XX 42 CNPISGNTLYMYRQ 56
XX
XX Db
XX
XX RESULT 10
XX AAR26969
XX ID AAR26969 standard; protein; 79 AA.
XX
XX AAR26969;
XX
XX 25-MAR-2003 (revised)
XX 11-FEB-1993 (first entry)
XX
XX Human T lymphocyte receptor V-beta 6 subfamily segment.
XX
XX TCR; IGR b 12; variable region; immunomodulation;
XX polymerase chain reaction; T cell receptor.
XX
XX Homo sapiens.
XX
XX WO9213950-A2.
XX
XX 20-AUG-1992.
XX
XX 12-FEB-1992; 92WO-FR000130.
XX
XX 12-FEB-1991; 91FR-00001613.
XX 12-APR-1991; 91FR-00004523.
XX
XX (ROUS ) ROUSSEL-UCIAF.
XX
XX Hercend T, Triebel F, Roman-Roman S, Ferradini L;
XX
XX WPI; 1992-300036/36.
XX N-PSDB; AAQ28182.
XX
XX Variable regions of b-chain of T-lymphocyte receptors and their DNA -
XX useful as immuno:modulant(s) and for diagnosing immune disorders.
XX
XX Claim 7; Page 46; 75pp; French.
XX

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XX RNA was isolated from peripheral lymphocytes and converted to cDNA using
CC a C-beta-specific primer. The cDNA was amplified by anchored PCR using C-
CC beta and polyC primers, then amplified again using a different C-beta
CC specific primer. The amplified product was SacII- restricted, inserted
CC into Bluescript SK+ vector and used to transform E.coli XL-1blue.
CC Transformants were screened with a C-beta specific probe and DNA from
CC positive clones was sequenced in the C-beta region. The sequence
CC designated "IGR b 12" represents a new member of the V beta 6 subfamily
CC and has a homology of 94% with three previously identified members of the
CC V beta 6 subfamily. The peptide encoded by it can be used to block T cell
CC epitopes and in vaccines. See also AAQ28173-Q28228. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 79 AA;

Query Match 77.1%; Score 74; DB 2; Length 79;
Best Local Similarity 68.8%; Pred. No. 0.00033;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CKPISGHSNLFMYROT 16
| | | | | : | | | | | :
| | | | | : | | | | | :
Db 7 CDPISGHSNLFMYROT 22

RESULT 11

AA65454
ID AA65454 standard; protein; 92 AA.

XX AAR65454;

XX 25-MAR-2003 (revised)

XX 24-MAY-1995 (first entry)

XX T-cell receptor V-beta HUVB6.9.

XX T-cell receptor; TCR; T-lymphocyte receptor; variable region; beta-chain;
XX V-beta; multiple sclerosis; cerebrospinal fluid; autoimmune disease;
XX lymphoma; vaccine.

XX Homo sapiens.

XX WO9425063-A1.

XX 10-NOV-1994.

XX 29-APR-1994; 94WO-US004789.

XX 29-APR-1993; 93US-00055006.

XX (IMMU-) IMMUNE RESPONSE CORP.

XX (SAND-) SAN DIEGO REGIONAL CANCER CENT.

XX Brostoff SW, Wilson DB, Smith LR, Gold DP, Carlo DJ;

XX WPI; 1994-357913/44.

XX New vaccine against multiple sclerosis using T-cell receptors - or
XX fragments of T-cell receptors from the beta chain variable region; for
XX treating autoimmune disease and lymphoma(s).

XX Disclosure; Fig 2A; 43pp; English.

XX Sequences of the T-cell receptor beta-chain variable region that were
XX most frequently expressed in cultures from the cerebrospinal fluid of
XX multiple sclerosis patients are given in AAR65450-67. A peptide based on
XX AAR65450-57 has been used for vaccine development. (Updated on 25-MAR-
XX 2003 to correct PN field.)

XX Sequence 92 AA;

Query Match 77.1%; Score 74; DB 2; Length 92;
Best Local Similarity 75.0%; Pred. No. 0.00039;

Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 CKPISGHSNLFMYROT 16
| | | | | : | | | | | :
| | | | | : | | | | | :
Db 21 CDPISGHSNLFMYROT 36

RESULT 12

AA73521
ID AA73521 standard; protein; 93 AA.

XX AA73521;

XX 02-SEP-1999 (first entry)

XX Amino acid sequence of human V beta 6.9.

XX Vaccine; T cell receptor; TCR; T cell; V beta 6.2/3; V beta 6/5;
XX V beta 6.7; V beta 2; V beta 5/1; V beta 7; V beta 13; V beta 6;
XX multiple sclerosis.

XX Homo sapiens.

XX WO927957-A1.

XX 10-JUN-1999.

XX 03-DEC-1997; 97WO-US023147.

XX 03-DEC-1997; 97WO-US023147.

XX (IMMU-) IMMUNE RESPONSE CORP.

XX (KIMM-) KIMMEL CANCER CENT SIDNEY.

XX Brostoff SW, Wilson DB, Smith LR, Gold DP, Carlo DJ;

XX WPI; 1999-404801/34.

XX T0 cell receptor peptide-derived vaccines.

XX Example 8; Fig 2A-B; 104pp; English.

XX The specification describes vaccines which comprise immunologically
XX effective amounts of T cell receptor (TCR) peptides. The TCRs are present
XX on the surface of T cells. The TCRs are chosen from V beta 6.2/3, V beta
XX 6/5, V beta 6.7, V beta 2, V beta 5/1, V beta 7 or V beta 13. The V beta
XX TCR peptide-based vaccines are useful for prevention or treatment of
XX multiple sclerosis (MS). The presence of V beta 6.7 appears to be
XX particularly associated with multiple sclerosis and can be used to
XX determine an individual's susceptibility to multiple sclerosis.
XX Vaccinating, rather than passively administering heterologous antibodies,
XX allows the host's own immune system to mobilize and suppress auto
XX aggressive T cells. Therefore, the suppression is persistent and may
XX involve any and all immunological mechanisms in effecting that
XX suppression. Such a multi-faceted response is more effective than the uni
XX -dimensional suppression achieved by passive administration of monoclonal
XX antibodies or extant-derived regulatory T cell clones. AA73517-34
XX represent human V beta proteins that are most frequently expressed in the
XX cerebrospinal fluid (CSF) of MS patients

XX Sequence 93 AA;

Query Match 77.1%; Score 74; DB 2; Length 93;
Best Local Similarity 75.0%; Pred. No. 0.0004;

Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CKPISGHSNLFMYROT 16
| | | | | : | | | | | :
| | | | | : | | | | | :
Db 21 CDPISGHSNLFMYROT 36

RESULT 13

AA78686

1D AAR78686 standard; protein; 94 AA.
XX
AC AAR78686;
XX
DT 12-APR-1996 (first entry)
XX
DE T-cell receptor beta-chain variable region V-beta-6.1.
XX
KM Diabetes; immunotherapy; T-cell receptor beta-chain.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 46..59
FT /label= CDR2
FT /note= "Claim 7, page 27"
XX
PV WO9521623-A1.
XX
PD 17-AUG-1995.
XX
PF 10-FEB-1995; 95WO-US001572.
XX
PR 14-FEB-1994; 94US-00195963.
XX
PS (UYVE-) UNIV VERMONT.
XX
PI Albertini RJ, Falta MT;
XX
DR WPI; 1995-292941/38.
XX
DR N-PSDB; AAQ96132.
XX
PT Preventing or reducing severity of diabetes - by inhibiting the activity
PT of specific T-cells, partic. by interfering with diabetes-associated T
PT cell receptors.
XX
PS Claim 4; Fig 1; 42pp; English.
XX
CC Non-conserved regions of T-cell receptor (TCR) beta-chain variable
CC regions V-beta-6.1, V-beta-6.6/6.7 and V-beta-14 (AAR78686-88) are used
CC in the prevention or therapy of diabetes. Diabetes is characterised by
CC predominant usage of TCRs bearing V-beta-6 and V-beta-14. Such TCRs can
CC be administered to a patient to generate an immune reaction that
CC neutralises or kills V-beta-bearing T-cells. Hypervariable CDR2 regions
CC (see AAR75364, AAR78689-90) of the V-beta-6 and V-beta-14 chains may also
CC be used
XX
SQ Sequence 94 AA;
XX
Query Match 77.1%; Score 74; DB 2; Length 94;
Best Local Similarity 68.8%; Pred. No. 0.0004;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 CKPISGNSLFWYRQT 16
DB 23 CDPISGHTALYMYRQS 38
XX
RESULT 14
ID AAR78687
XX
AC AAR78687;
XX
DT 12-APR-1996 (first entry)
XX
DE T-cell receptor beta-chain variable region V-beta-6.6/6.7.
XX
KM Diabetes; immunotherapy; T-cell receptor beta-chain.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers

FT Region 48..61
FT /label= CDR2
FT /note= "Claim 8, page 28"
XX
PN WO9521623-A1.
XX
PD 17-AUG-1995.
XX
PF 10-FEB-1995; 95WO-US001572.
XX
PR 14-FEB-1994; 94US-00195963.
XX
PS (UYVE-) UNIV VERMONT.
XX
PI Albertini RJ, Falta MT;
XX
DR WPI; 1995-292941/38.
XX
DR N-PSDB; AAQ96133.
XX
PT Preventing or reducing severity of diabetes - by inhibiting the activity
PT of specific T-cells, partic. by interfering with diabetes-associated T
PT cell receptors.
XX
PS Claim 4; Fig 1; 42pp; English.
XX
CC Non-conserved regions of T-cell receptor (TCR) beta-chain variable
CC regions V-beta-6.1, V-beta-6.6/6.7 and V-beta-14 (AAR78686-88) are used
CC in the prevention or therapy of diabetes. Diabetes is characterised by
CC predominant usage of TCRs bearing V-beta-6 and V-beta-14. Such TCRs can
CC be administered to a patient to generate an immune reaction that
CC neutralises or kills V-beta-bearing T-cells. Hypervariable CDR2 regions
CC (see AAR75364, AAR78689-90) of the V-beta-6 and V-beta-14 chains may also
CC be used
XX
SQ Sequence 96 AA;
XX
Query Match 77.1%; Score 74; DB 2; Length 96;
Best Local Similarity 68.8%; Pred. No. 0.00041;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 CKPISGNSLFWYRQT 16
DB 24 CDPISGHTALYMYRQS 39
XX
RESULT 15
ID AAR65453
XX
AC AAR65453;
XX
DT 25-MAR-2003 (revised)
DT 24-MAY-1995 (first entry)
XX
DE T-cell receptor V-beta HVB6.5.
XX
KM T-cell receptor; TCR; T-lymphocyte receptor; variable region; beta-chain;
KM V-beta; multiple sclerosis; cerebrospinal fluid; autoimmune disease;
KM lymphoma; vaccine.
XX
OS Homo sapiens.
XX
PN WO9425063-A1.
XX
PD 10-NOV-1994.
XX
PF 29-APR-1994; 94WO-US004789.
XX
PR 29-APR-1993; 93US-00055006.
XX
PS (IMMU-) IMMUNE RESPONSE CORP.
PS (SAND-) SAN DIEGO REGIONAL CANCER CENT.
XX

PI Brostoff SW, Wilson DB, Smith LR, Gold DP, Carlo DJ;
 XX
 DR WPI, 1994-357913/44.
 XX
 PT New vaccine against multiple sclerosis using T-cell receptors - or
 PT fragments of T-cell receptors from the beta chain variable region; for
 PT treating auto-immune disease and lymphoma(s).
 XX
 PS Disclosure; Fig 2A, 43pp; English.
 XX
 CC Sequences of the T-cell receptor beta-chain variable region that were
 CC most frequently expressed in cultures from the cerebrospinal fluid of
 CC multiple sclerosis patients are given in AAR65450-67. A peptide based on
 CC AAR65450-57 has been used for vaccine development. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX
 SQ Sequence 104 AA;

Query Match 77.1%; Score 74; DB 2; Length 104;
 Best Local Similarity 75.0%; Pred. No. 0.00045;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CKPSGHNLSFWYRQT 16
 DB 33 CDPISSEHRLWYRQT 48

Search completed: March 5, 2004, 16:34:50
 Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 5, 2004, 16:33:50 ; Search time 23 Seconds
(without alignments) 35,914 Million cell updates/sec

Title: US-09-591-789-1

Sequence: 1 CKPISGNSLFWYRQT 16

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	16	2	US-08-696-049-1
2	96	100.0	75	4	US-09-050-861B-7
3	96	100.0	102	3	US-08-466-368-9
4	96	100.0	102	4	US-08-470-998-6
5	96	100.0	102	4	US-08-328-500-14
6	74	77.1	93	4	US-08-055-006-17
7	74	77.1	106	4	US-08-055-006-15
8	74	77.1	106	4	US-08-055-006-16
9	74	77.1	114	4	US-08-055-006-12
10	74	77.1	114	4	US-08-055-006-18
11	74	77.1	114	4	US-08-055-006-19
12	74	77.1	310	3	US-08-897-097-4
13	74	77.1	311	3	US-08-897-097-3
14	74	77.1	314	3	US-08-897-097-1
15	73	76.0	114	4	US-08-055-006-14
16	72	75.0	114	4	US-08-055-006-13
17	70	72.9	114	4	US-08-055-006-31
18	69	71.9	114	4	US-08-055-006-20
19	66	68.8	94	4	US-08-055-006-21
20	65	67.7	92	1	US-08-181-492B-27
21	65	67.7	92	5	PCT-US93-00408-27
22	56	58.3	82	1	US-08-476-405A-25
23	56	58.3	121	3	US-08-341-560B-4
24	56	58.3	121	4	US-08-353-940-4
25	56	58.3	121	4	US-10-163-127-4
26	56	58.3	121	5	PCT-US93-03895-4
27	56	58.3	250	3	US-08-341-560B-6

28	56	58.3	250	4	US-08-353-940-6	Sequence 6, Appl
29	56	58.3	250	4	US-10-162-127-6	Sequence 6, Appl
30	56	58.3	250	5	PCT-US93-03895-6	Sequence 6, Appl
31	56	58.3	306	3	US-09-082-593-2	Sequence 2, Appl
32	54	56.2	94	4	US-08-055-006-24	Sequence 24, Appl
33	49	51.0	94	4	US-08-055-006-26	Sequence 26, Appl
34	49	51.0	106	4	US-08-442-001C-74	Sequence 74, Appl
35	48	50.0	77	4	US-08-055-006-27	Sequence 27, Appl
36	47	49.0	18	1	US-08-476-405A-1	Sequence 1, Appl
37	47	49.0	94	3	US-08-297-395-10	Sequence 10, Appl
38	47	49.0	94	4	US-08-182-967-3	Sequence 3, Appl
39	47	49.0	106	2	US-08-652-558-1	Sequence 1, Appl
40	47	49.0	113	3	US-08-466-860-7	Sequence 7, Appl
41	47	49.0	113	3	US-08-472-040A-7	Sequence 7, Appl
42	47	49.0	113	3	US-08-276-776-7	Sequence 7, Appl
43	47	49.0	113	3	US-08-471-208-7	Sequence 7, Appl
44	47	49.0	154	1	US-08-246-242-7	Sequence 7, Appl
45	47	49.0	303	4	US-09-509-347-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-696-049-1
Sequence 1, Application US/08696049
Patent No. 5911990
GENERAL INFORMATION:
APPLICANT: Marchaloni, John J.
APPLICANT: Watson, Ronald R.
APPLICANT: Denghanpishah, Keivan
APPLICANT: Wang, Yuejian
APPLICANT: Huang, Dennis S.
TITLE OF INVENTION: T-Cell Receptor Peptides and Methods for Preventing the Progression to AIDS in an Animal Model
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,049
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: ARIZ:002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/787-1400
TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-696-049-1
Query Match 100.0%; Score 96; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 CKPISGNSLFWYRQT 16

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Db      1 CKPISGNSLFWYRQT 16

RESULT 2
US-09-050-861B-7
; Sequence 7, Application US/09050861B
; Patent No. 6555314
; GENERAL INFORMATION:
; APPLICANT: Payan, Donald
; TITLE OF INVENTION: TOSO AS A TARGET FOR DRUG SCREENING
; FILE REFERENCE: RIGL-002CON
; CURRENT APPLICATION NUMBER: US/09/050,861B
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: US/09/651,150B
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: US 09/050,861
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-050-861B-7

Query Match      100.0%; Score 96; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 7.2e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CKPISGNSLFWYRQT 16
Db      5 CKPISGNSLFWYRQT 20

RESULT 3
US-08-466-368-9
; Sequence 9, Application US/08466368
; Patent No. 6093539
; GENERAL INFORMATION:
; APPLICANT: Maddon, Paul J.
; APPLICANT: Littman, Dan R.
; APPLICANT: Chess, Leonard
; APPLICANT: Axel, Richard
; APPLICANT: Weiss, Robin
; APPLICANT: McDougal, J. S.
; TITLE OF INVENTION: DNA ENCODING THE T CELL SURFACE PROTEIN
; TITLE OF INVENTION: T4 AND USE OF FRAGMENTS OF T4 IN THE TREATMENT OF AIDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,368
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 24577-El-B/JPM/ACC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FEATURE:
; NAME/KEY: Active-site
; LOCATION: 1..102
US-08-466-368-9

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Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CKPISGNSLFWYRQT 16
Db      23 CKPISGNSLFWYRQT 38

RESULT 4
US-08-470-998-6
; Sequence 6, Application US/08470998
; Patent No. 6570000
; GENERAL INFORMATION:
; APPLICANT: Maddon, Paul J.
; APPLICANT: Littman, Dan R.
; APPLICANT: Chess, Leonard
; APPLICANT: Axel, Richard
; APPLICANT: Weiss, Robin
; APPLICANT: McDougal, J. S.
; TITLE OF INVENTION: DNA ENCODING THE T CELL SURFACE PROTEIN
; TITLE OF INVENTION: T4 AND USE OF FRAGMENTS OF T4 IN THE TREATMENT OF AIDS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,998
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 24577-Fl-B/JPM/ACC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FEATURE:
; NAME/KEY: Active-site
; LOCATION: 1..102
US-08-470-998-6
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Query Match 100.0%; Score 96; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYROT 16
| | | | | | | | | | | | | | | | | |
DB 23 CKPISGNSLFWYROT 38

RESULT 5

US-08-328-500-14
; Sequence 14, Application US/08328500
; Patent No. 6673836
; GENERAL INFORMATION:
; APPLICANT: Maddon, Paul J.
; APPLICANT: Axel, Richard
; APPLICANT: Sweet, Richard W.
; APPLICANT: Athos, James
; TITLE OF INVENTION: DERIVATIVES OF SOLUBLE T-4
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,500
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET INFORMATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-328-500-14

Query Match 100.0%; Score 96; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYROT 16
| | | | | | | | | | | | | | | | | |
DB 23 CKPISGNSLFWYROT 38

RESULT 6
US-08-055-006-17
; Sequence 17, Application US/08055006
; Patent No. 6464978
; GENERAL INFORMATION:
; APPLICANT: Brostoff, Steven W.

; APPLICANT: Wilson, Darcy B.
; SMITH, Lawrence R.
; Gold, Daniel P.
; Carlo, Dennis J.
; TITLE OF INVENTION: Vaccination and Methods Against Multiple
; Sclerosis Resulting From Pathogenic Responses By Specific T

Cell Populations
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/055,006
FILING DATE: 09-Feb-1993
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 9611
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-055-006-17

Query Match 77.1%; Score 74; DB 4; Length 93;
Best Local Similarity 75.0%; Pred. No. 4.2e-05;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYROT 16
| | | | | | | | | | | | | | | | | |
DB 21 CDPISGNSLFWYROT 36

RESULT 7
US-08-055-006-15
; Sequence 15, Application US/08055006
; Patent No. 6464978
; GENERAL INFORMATION:
; APPLICANT: Brostoff, Steven W.

; APPLICANT: Wilson, Darcy B.
; SMITH, Lawrence R.
; Gold, Daniel P.
; Carlo, Dennis J.
; TITLE OF INVENTION: Vaccination and Methods Against Multiple
; Sclerosis Resulting From Pathogenic Responses By Specific T
; Cell Populations

NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/055,006
FILING DATE: 09-Feb-1993
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1M 9611
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-08-055-006-15

Query Match 77.1%; Score 74; DB 4; Length 106;
Best Local Similarity 75.0%; Pred. No. 4.8e-05;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CKPIGHSNLFMYRQT 16
DB 34 CDPISHNRLYMYRQT 49

RESULT 8
US-08-055-006-16
Sequence 16, Application US/08055006
Patent No. 6464978
GENERAL INFORMATION:
APPLICANT: Brostoff, Steven W.
Wilson, Darcy B.
Smith, Lawrence R.
Gold, Daniel P.
Carlo, Dennis J.
TITLE OF INVENTION: Vaccination and Methods Against Multiple
Sclerosis Resulting From Pathogenic Responses By Specific T
Cell Populations
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/055,006
FILING DATE: 09-Feb-1993
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1M 9611
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-9001
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-08-055-006-16

Query Match 77.1%; Score 74; DB 4; Length 106;
Best Local Similarity 75.0%; Pred. No. 4.8e-05;

Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CKPIGHSNLFMYRQT 16
DB 34 CDPISHNRLYMYRQT 49

RESULT 9
US-08-055-006-12
Sequence 12, Application US/08055006
Patent No. 6464978
GENERAL INFORMATION:
APPLICANT: Brostoff, Steven W.
Wilson, Darcy B.
Smith, Lawrence R.
Gold, Daniel P.
Carlo, Dennis J.
TITLE OF INVENTION: Vaccination and Methods Against Multiple
Sclerosis Resulting From Pathogenic Responses By Specific T
Cell Populations
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/055,006
FILING DATE: 09-Feb-1993
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1M 9611
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-08-055-006-12

Query Match 77.1%; Score 74; DB 4; Length 114;
Best Local Similarity 68.8%; Pred. No. 5.2e-05;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CKPIGHSNLFMYRQT 16
DB 42 CDPISGHTALYMYRQS 57

RESULT 10
US-08-055-006-18
Sequence 18, Application US/08055006
Patent No. 6464978
GENERAL INFORMATION:
APPLICANT: Brostoff, Steven W.
Wilson, Darcy B.
Smith, Lawrence R.
Gold, Daniel P.
Carlo, Dennis J.
TITLE OF INVENTION: Vaccination and Methods Against Multiple

Sclerosis Resulting From Pathogenic Responses By Specific T
Cell Populations
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/055,006
FILING DATE: 09-Feb-1993
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 9611
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-08-055-006-18
Query Match 77.1%; Score 74; DB 4; Length 114;
Best Local Similarity 68.8%; Pred. No. 5.2e-05;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 CKPISGNSLFWYRQT 16
| | | | | : | | | | | :
| | | | | : | | | | | :
Db 42 CDPISGHTALWYRQS 57
RESULT 11
US-08-055-006-19
Sequence 19, Application US/08055006
Patent No. 6464978
GENERAL INFORMATION:
APPLICANT: Brostoff, Steven W.
Wilson, Darcy B.
Smith, Lawrence R.
Gold, Daniel P.
Carlo, Dennis J.
TITLE OF INVENTION: Vaccination and Methods Against Multiple
Sclerosis Resulting From Pathogenic Responses By Specific T
Cell Populations
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/055,006
FILING DATE: 09-Feb-1993

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 9611
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-08-055-006-19
Query Match 77.1%; Score 74; DB 4; Length 114;
Best Local Similarity 68.8%; Pred. No. 5.2e-05;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 CKPISGNSLFWYRQT 16
| | | | | : | | | | | :
| | | | | : | | | | | :
Db 42 CDPISGHTALWYRQS 57
RESULT 12
US-08-897-097-4
Sequence 4, Application US/08897097
Patent No. 6054292
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Corley, Neil C.
TITLE OF INVENTION: T-CELL RECEPTOR BETA-LIKE PROTEIN
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,097
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0346 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 339012
US-08-897-097-4

Query Match 77.1%; Score 74; DB 3; Length 310;
Best Local Similarity 75.0%; Pred. No. 0.00015;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYRQT 16
DB 42 CDPISGNSLFWYRQT 57

RESULT 13
US-08-897-097-3
Sequence 3, Application US/08897097
Patent No. 6054292
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: T-CELL RECEPTOR BETA-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,097
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0346 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1100182
US-08-897-097-3
Query Match 77.1%; Score 74; DB 3; Length 311;
Best Local Similarity 75.0%; Pred. No. 0.00015;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYRQT 16
DB 42 CDPISGNSLFWYRQT 57

RESULT 14
US-08-897-097-1
Sequence 1, Application US/08897097
Patent No. 6054292
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: T-CELL RECEPTOR BETA-LIKE PROTEIN

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,097
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0346 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TONGTUT01
CLONE: 983910
US-08-897-097-1
Query Match 77.1%; Score 74; DB 3; Length 314;
Best Local Similarity 68.8%; Pred. No. 0.00016;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYRQT 16
DB 42 CDPISGNSLFWYRQT 57

RESULT 15
US-08-055-006-14
Sequence 14, Application US/08055006
Patent No. 6464978
GENERAL INFORMATION:
APPLICANT: Brostoff, Steven W.
 Wilson, Darcy B.
 Smith, Lawrence R.
 Gold, Daniel P.
 Carlo, Dennis J.
TITLE OF INVENTION: Vaccination and Methods Against Multiple
 Sclerosis Resulting From Pathogenic Responses By Specific T
 Cell Populations
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/055,006
;   FILING DATE: 09-Feb-1993
;   CLASSIFICATION: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Campbell, Cathryn A.
;     REGISTRATION NUMBER: 31,815
;     REFERENCE/DOCKET NUMBER: P-1M 9611
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (619)535-9001
;     TELEFAX: (619)535-8949
;   INFORMATION FOR SEQ ID NO: 14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 114 amino acids
;       TYPE: amino acid
;       TOPOLOGY: unknown
;     MOLECULE TYPE: protein
;     SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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; US-08-055-006-14

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Query Match      76.0%; Score 73; DB 4; Length 114;
Best Local Similarity 80.0%; Pred. No. 7,6e-05;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 CKPIGSHNSLFWYRQ 15
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Db      42 CDPISGHVSLTYWYRQ 56

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Search completed: March 5, 2004, 16:37:22
 Job time : 30 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 5, 2004, 16:36:16 ; Search time 34 Seconds
(without alignments)
99.366 Million cell updates/sec

Title: US-09-591-789-1
Percent score: 96
Sequence: 1 CKPISGNSLFWYRQT 16

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 809742 seqs, 21153259 residues
Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/prodata/1/pubppa/US06_PUB_PUB.pep.*
 - 3: /cgn2_6/prodata/1/pubppa/US06_PUB_PUB.pep.*
 - 4: /cgn2_6/prodata/1/pubppa/US07_PUB_PUB.pep.*
 - 5: /cgn2_6/prodata/1/pubppa/US07_PUB_PUB.pep.*
 - 6: /cgn2_6/prodata/1/pubppa/US08_PUB_PUB.pep.*
 - 7: /cgn2_6/prodata/1/pubppa/US08_PUB_PUB.pep.*
 - 8: /cgn2_6/prodata/1/pubppa/US08_PUB_PUB.pep.*
 - 9: /cgn2_6/prodata/1/pubppa/US08_PUB_PUB.pep.*
 - 10: /cgn2_6/prodata/1/pubppa/US09_PUB_PUB.pep.*
 - 11: /cgn2_6/prodata/1/pubppa/US09_PUB_PUB.pep.*
 - 12: /cgn2_6/prodata/1/pubppa/US09_PUB_PUB.pep.*
 - 13: /cgn2_6/prodata/1/pubppa/US10_PUB_PUB.pep.*
 - 14: /cgn2_6/prodata/1/pubppa/US10_PUB_PUB.pep.*
 - 15: /cgn2_6/prodata/1/pubppa/US10_PUB_PUB.pep.*
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 - 18: /cgn2_6/prodata/1/pubppa/US60_PUB_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	95	9	US-09-263-959-1189
2	96	100.0	102	11	US-09-891-119A-14
3	96	100.0	115	9	US-09-263-959-323
4	85	88.5	115	9	US-09-263-959-324
5	82	85.4	113	9	US-09-263-959-326
6	80	83.3	113	9	US-09-263-959-325
7	75	78.1	113	9	US-09-263-959-1212
8	74	77.1	94	9	US-09-263-959-1187
9	74	77.1	115	9	US-09-263-959-311
10	74	77.1	115	9	US-09-263-959-314
11	74	77.1	115	10	US-09-327-122-25
12	73.5	76.6	84	9	US-09-135-2388-7
13	73	76.0	115	9	US-09-263-959-313
14	73	76.0	115	9	US-09-263-959-315
15	73	76.0	115	9	US-09-263-959-352

16	72	75.0	115	9	US-09-263-959-312	Sequence 312, App
17	72	75.0	115	9	US-09-263-959-316	Sequence 316, App
18	71	74.0	99	9	US-09-263-959-1202	Sequence 1202, App
19	71	74.0	115	9	US-09-263-959-350	Sequence 350, App
20	70	72.9	97	9	US-09-263-959-1186	Sequence 1186, App
21	70	72.9	98	9	US-09-263-959-1197	Sequence 1197, App
22	70	72.9	114	9	US-09-263-959-304	Sequence 304, App
23	70	72.9	114	9	US-09-263-959-310	Sequence 310, App
24	70	72.9	115	9	US-09-263-959-345	Sequence 345, App
25	70	72.9	287	9	US-09-912-787-61	Sequence 61, App1
26	70	72.9	287	9	US-09-912-787-65	Sequence 65, App1
27	70	72.9	287	13	US-10-014-346-47	Sequence 47, App1
28	70	72.9	287	13	US-10-014-346-51	Sequence 51, App1
29	68	70.8	115	9	US-09-263-959-351	Sequence 351, App
30	67	69.8	113	9	US-09-263-959-318	Sequence 318, App
31	67	69.8	115	9	US-09-263-959-317	Sequence 317, App
32	66	68.8	114	9	US-09-263-959-307	Sequence 307, App
33	65	67.7	96	9	US-09-263-959-1206	Sequence 1206, App
34	65	67.7	114	9	US-09-263-959-306	Sequence 306, App
35	63	65.6	115	9	US-09-263-959-1199	Sequence 1199, App
36	63	65.6	115	9	US-09-263-959-347	Sequence 347, App
37	61	63.5	115	9	US-09-263-959-319	Sequence 319, App
38	59	61.5	91	9	US-09-263-959-1211	Sequence 1211, App
39	58	61.5	108	9	US-09-263-959-1213	Sequence 1213, App
40	58	60.4	114	9	US-09-263-959-305	Sequence 305, App
41	57.5	59.9	114	9	US-09-263-959-356	Sequence 356, App
42	56	58.3	60	9	US-09-864-761-37676	Sequence 37676, A
43	56	58.3	98	9	US-09-263-959-1203	Sequence 1203, App
44	56	58.3	114	9	US-09-263-959-321	Sequence 321, App
45	56	58.3	114	9	US-09-263-959-322	Sequence 322, App

ALIGNMENTS

RESULT 1
US-09-263-959-1189
Sequence 1189, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: KOOP, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1189:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-09-263-959-1189

Query Match 100.0%; Score 96; DB 9; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYROT 16
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DB 22 CKPISGNSLFWYROT 37

RESULT 2

US-09-891-119A-14
; Sequence 14, Application US/09891119A
; Publication No. US20040013683A1
; GENERAL INFORMATION:
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: DERIVATIVES OF SOLUBLE T-4
; FILE REFERENCE: 24577-CY-B
; CURRENT FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 14
; LENGTH: 102
; TYPE: PRT
; ORGANISM: human
US-09-891-119A-14

Query Match 100.0%; Score 96; DB 11; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYROT 16
|||||
DB 23 CKPISGNSLFWYROT 38

RESULT 3

US-09-263-959-323
; Sequence 323, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263.959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4800
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 323:
SEQUENCE CHARACTERISTICS:

LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-263-959-323

Query Match 100.0%; Score 96; DB 9; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYROT 16
|||||
DB 42 CKPISGNSLFWYROT 57

RESULT 4

US-09-263-959-324
; Sequence 324, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263.959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 324:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-263-959-324

Query Match 88.5%; Score 85; DB 9; Length 115;
Best Local Similarity 87.5%; Pred. No. 9.7e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYROT 16
|||||
DB 42 CKPISGNSLFWYROT 57

RESULT 5

US-09-263-959-326
; Sequence 326, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Seed and Berry LLP
;; STREET: 6300 Columbia Center, 701 Fifth Avenue
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: US
;; ZIP: 98104-7092
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/263,959
;; FILING DATE: 05-MAR-1999
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McMasters, David D.
;; REGISTRATION NUMBER: 33,963
;; TELECOMMUNICATION INFORMATION:
;; REFERENCE/DOCKET NUMBER: 920010.426C2
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 325:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 113 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; US-09-263-959-326

Query Match 85.4%; Score 82; DB 9; Length 113;
Best Local Similarity 81.2%; Pred. No. 2.8e-05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CKPIGHSNLFMYROT 16
Db 41 CEPISGNDLWYROT 56

RESULT 6
US-09-263-959-325
; Sequence 325, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 325:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-263-959-325

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 115 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; US-09-263-959-325

Query Match 83.3%; Score 80; DB 9; Length 115;
Best Local Similarity 75.0%; Pred. No. 5.9e-05;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKPIGHSNLFMYROT 16
Db 42 CQPIGHNTVFWYROT 57

RESULT 7
US-09-263-959-1212
; Sequence 1212, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1212:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-263-959-1212

Query Match 78.1%; Score 75; DB 9; Length 113;
Best Local Similarity 75.0%; Pred. No. 0.00035;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CKPIGHSNLFMYROT 16
Db 41 CEPISGNDLWYROT 56

RESULT 8
US-09-263-959-1187
; Sequence 1187, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1187:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-263-959-1187

Query Match 77.1%; Score 74; DB 9; Length 94;
Best Local Similarity 68.8%; Pred. No. 0.00042;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CKPISGHSLEFWYROT 16
DB 22 CDPISGHTALYMYRQS 37

RESULT 9
US-09-263-959-311
Sequence 311, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 311:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-263-959-311

INFORMATION FOR SEQ ID NO: 311:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-263-959-311

Query Match 77.1%; Score 74; DB 9; Length 115;
Best Local Similarity 68.8%; Pred. No. 0.00051;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CKPISGHSLEFWYROT 16
DB 42 CDPISGHTALYMYRQS 57

RESULT 10
US-09-263-959-314
Sequence 314, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 314:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-263-959-314

Query Match 77.1%; Score 74; DB 9; Length 115;
Best Local Similarity 75.0%; Pred. No. 0.00051;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CKPISGHSLEFWYROT 16
DB 42 CDPISGHTALYMYRQS 57

RESULT 11
US-09-927-122-25
Sequence 25, Application US/09927122
Publication No. US20030012782A1
GENERAL INFORMATION:
APPLICANT: GOLD, DANIEL P.
APPLICANT: SHOPE, ROBERT J.
TITLE OF INVENTION: METHOD AND COMPOSITION FOR ALTERING A T CELL MEDIATED

```

; TITLE OF INVENTION: PATHOLOGY
; FILE REFERENCE: 032077.0002
; CURRENT APPLICATION NUMBER: US/09/927,122
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 25
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: TCR beta chain
US-09-927-122-25

Query Match
Best Local Similarity 77.1%; Score 74; DB 10; Length 311;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CKPIGSHNSLFWYRQT 16
DB 42 CDPISEHNRILVYRQT 57

RESULT 12
US-09-135-238B-7
; Sequence 7, Application US/09135238B
; Patent No. US20020177555A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020177555A1an, Garry F.
; APPLICANT: Hiroshi, Yasumichi
; TITLE OF INVENTION: TOSO
; FILE REFERENCE: A65635-1/DJB/RMS
; CURRENT APPLICATION NUMBER: US/09/135,238B
; CURRENT FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/066,063
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 7
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (11)..(14)
; OTHER INFORMATION: The xaa at positions 11 through 14 represents an
; OTHER INFORMATION: unknown amino acid.
; NAME/KEY: UNSURE
; LOCATION: (18)
; OTHER INFORMATION: The xaa at position 18 represents an unknown amino
; OTHER INFORMATION: acid.
; NAME/KEY: UNSURE
; LOCATION: (28)
; OTHER INFORMATION: The xaa at position 28 represents an unknown amino
; OTHER INFORMATION: acid.
; NAME/KEY: UNSURE
; LOCATION: (59)..(61)
; OTHER INFORMATION: The xaa at positions 59 through 61 represents an
; OTHER INFORMATION: unknown amino acid.
US-09-135-238B-7

Query Match
Best Local Similarity 76.6%; Score 73.5; DB 9; Length 84;
Matches 16; Conservative 0; Mismatches 0; Indels 5; Gaps 2;

QY 1 CKPIGSHNSLFWYRQT 16
DB 5 CKPIGSHNSLFWYRQT 25

RESULT 13
US-09-263-959-313
; Sequence 313, Application US/09263959
```

```

; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

US-09-263-959-313

Query Match
Best Local Similarity 76.0%; Score 73; DB 9; Length 115;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CKPIGSHNSLFWYRQ 15
DB 42 CDPIGSHVSLFWYRQ 56

RESULT 14
US-09-263-959-315
; Sequence 315, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
```

NAME: McMaisters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 920010.426C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 315:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 115 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-09-263-959-315

Query Match 76.0%; Score 73; DB 9; Length 115;
 Best Local Similarity 73.3%; Pred. No. 0.00073;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CKPISGHSLEFWYRQ 15
 |||||:||||
 Db 42 CDPISGHTALWYRQ 56

RESULT 15

US-09-263-959-352
 Sequence 352, Application US/09263959
 Patent No. US20020150891A1
 GENERAL INFORMATION:
 APPLICANT: Hood, Leroy E.
 APPLICANT: Rowen, Lee
 APPLICANT: Koop, Ben F.
 TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 NUMBER OF SEQUENCES: 1279
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Seed and Berry LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/263,959
 FILING DATE: 05-MAR-1999
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: McMaisters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 920010.426C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 352:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 115 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-09-263-959-352

Query Match 76.0%; Score 73; DB 9; Length 115;
 Best Local Similarity 73.3%; Pred. No. 0.00073;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CKPISGHSLEFWYRQ 15
 |||||:||||
 Db 42 CDPISGHTALWYRQ 56

Search completed: March 5, 2004, 16:41:39
 Job time : 34 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 5, 2004, 16:30:45 ; Search time 21 Seconds

(without alignments)
73.289 Million cell updates/sec

Title: US-09-591-789-1

Perfect score: 96

Sequence: 1 CKPISGHNSLFWYRQT 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	114	2 I38314	T-cell receptor be
2	96	100.0	115	2 S03510	T-cell receptor be
3	96	100.0	135	1 RMWUY	T-cell receptor be
4	96	100.0	135	2 S57877	T-cell receptor CK
5	87	90.6	134	2 I71938	MHC class II I-A-b
6	85	88.5	93	2 S03488	T-cell receptor be
7	85	88.5	114	2 I38315	T-cell receptor be
8	85	88.5	115	2 S03511	T-cell receptor be
9	85	88.5	133	2 S57870	T-cell receptor CK
10	81	84.4	114	2 A27553	T-cell receptor be
11	81	84.4	134	1 RMWSB3	T-cell receptor be
12	81	84.4	145	2 S21651	T-cell receptor be
13	81	84.4	307	1 RMWSBC	T-cell receptor be
14	80	83.3	114	2 S17379	T-cell receptor be
15	80	83.3	114	2 I38316	T-cell receptor be
16	80	83.3	115	2 S03513	T-cell receptor be
17	77	80.2	115	2 A30995	T-cell receptor be
18	74	77.1	38	2 PLO229	T-cell receptor be
19	74	77.1	61	2 S30440	T-cell receptor be
20	74	77.1	79	2 S17389	T-cell receptor be
21	74	77.1	84	2 I38310	T-cell receptor be
22	74	77.1	91	2 PLO227	T-cell receptor be
23	74	77.1	93	2 A27590	T-cell receptor be
24	74	77.1	101	2 I32537	T-cell receptor be
25	74	77.1	106	2 H32537	T-cell receptor be
26	74	77.1	106	2 PTO733	T-cell receptor be
27	74	77.1	114	2 PTO734	T-cell receptor be
28	74	77.1	114	2 S17387	T-cell receptor be
29	74	77.1	115	2 S22035	T-cell receptor be

ALIGNMENTS

RESULT 1

I38314 T-cell receptor beta chain V region (V-beta 8.1, germline) precursor - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jan-2000

C/Accession: I38314

R/Slightom, J.L.; Siemieniuk, D.R.; Siu, L.C.; Koop, B.F.; Hood, L.

Genomics 20, 149-168, 1994

A/Title: Nucleotide sequence analysis of 77.7 kb of the human V beta T-cell receptor gen

A/Reference number: A54302; MID:94292194; PMID:8020962

A/Accession: I38314

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1-114 <RES>

A/Cross-references: EMBL:U03115; NID:G467918; PIDN:AAA17713.1; PID:G467923

C/Genetics:

A/Gene: TCRBV81

A/Intons: 17/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

F/35-113/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 96; DB 2; Length 114;

Best Local Similarity 100.0%; Pred. No. 2e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qx 1 CKPISGHNSLFWYRQT 16

Db 42 CKPISGHNSLFWYRQT 57

RESULT 2

S03510 T-cell receptor beta chain precursor V region (8.1) - human

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000

C/Accession: S03510; S03512

R/Siu, G.; Strause, E.C.; Lai, E.; Hood, L.E.

J. Exp. Med. 164, 1600-1614, 1986

A/Title: Analysis of a human V-beta gene subfamily.

A/Reference number: S03510; PMID:87035436; PMID:3772297

A/Accession: S03510

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-115 <SIU>

A/Cross-references: EMBL:X07192

A/Note: this sequence was determined from the germline gene

R/Smith, W.J.; Turncliffe, A.; Rabbitts, T.H.

Nucleic Acids Res. 15, 4991, 1987

A/Title: Germline sequence of two human T-cell receptor V-beta genes: V-beta-8.1 is tran

A/Reference number: S00520; MID:87259979; PMID:2955286

A/Accession: S03512

A:Molecule type: DNA
 A:Residues: 1-10 <SMI>
 A>Note: this sequence was determined from the germline gene
 C:Genetics:
 A:Insertions: 17/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: T-cell receptor
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:12-115/Product: T-cell receptor beta chain (fragment) #status predicted <MAT>
 F:12-115/Domain: V region (V-beta 8.1) #status predicted <VRE>
 F:35-113/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 96; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 2e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGNSLFMYRQT 16
 |||||
 DB 42 CKPISGNSLFMYRQT 57

RESULT 3

RHMYV
 T-cell receptor beta chain precursor V region (Y135) - human
 N:Alternate names: T-cell receptor beta-1 chain J-B1.2 segment
 C:Species: Homo sapiens (man)
 C>Date: 03-Aug-1994 #sequence_revision 03-Aug-1984 #text_change 22-Jun-1999
 C:Accession: A02000; E24687
 R:Yanagi, Y.; Yoshikai, Y.; Leggett, K.; Clark, S.P.; Aleksander, I.; Mak, T.W.
 Nature 308, 145-149, 1994
 A>Title: A human T cell-specific cDNA clone encodes a protein having extensive homology
 A:Reference number: A93324; MUID:84142269; PMID:6316315
 A:Accession: A02000

A:Molecule type: mRNA
 A:Residues: 1-135 <YAN>
 A:Cross-references: GB:K01571
 A:Experimental source: clone Y135
 R:Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
 A>Title: Organization and sequences of the diversity, joining, and constant region genes
 A:Reference number: A94081; MUID:86094276; PMID:3866244
 A:Accession: E24687
 A:Molecule type: DNA
 A:Residues: 121-135 <TOY>
 A:Cross-references: GB:M14158; NID:G338844; PIDN:AAA60669.1; PID:9553682
 C:Genetics:
 A:Gene: GDB:TCRB
 A:Cross-references: GDB:120405; OMIM:186930
 A:Map position: 7q35-7q35
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein; heterotrimer; receptor T-cell
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:12-115/Product: T-cell receptor beta chain V region Y135 #status predicted <MAT>
 F:35-113/Domain: immunoglobulin homology <IMM>
 F:42-111/Disulfide bonds: #status predicted
 F:90/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 96; DB 1; Length 135;
 Best Local Similarity 100.0%; Pred. No. 2.3e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGNSLFMYRQT 16
 |||||
 DB 42 CKPISGNSLFMYRQT 57

RESULT 4

S57877
 T cell receptor CK14 beta chain - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S57877
 R:Geigerich, G.; Pette, M.; Mehl, E.; Eppien, J.T.; Wekerle, H.; Hunkanner, A.

Eur. J. Immunol. 22, 753-758, 1992
 A>Title: Diversity of T cell receptor alpha and beta chain genes expressed by human T ce
 A:Reference number: S57869; MUID:92192091; PMID:1372258
 A:Accession: S57877
 A>Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-135 <GIE>
 A:Cross-references: EMBL:X58324; NID:9643002; PIDN:CAA41236.1; PID:9643003
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: T-cell receptor
 F:35-113/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 96; DB 2; Length 135;
 Best Local Similarity 100.0%; Pred. No. 2.3e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGNSLFMYRQT 16
 |||||
 DB 42 CKPISGNSLFMYRQT 57

RESULT 5

MHC class II I-A-beta protein precursor - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
 C:Accession: J11938
 R:Spitelia, D.G.; Hansen, T.H.; Walsh, W.D.; Behlke, M.A.; Tillinghast, J.P.; Chou, H.S.
 J. Immunol. 138, 3991-3995, 1987
 A>Title: Receptor diversity of insulin-specific T cell lines from C57BL (H-2b) mice.
 A:Reference number: 155978; MUID:87224052; PMID:3293795
 A:Accession: J11938
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-134 <RES>
 A:Cross-references: GB:M16681; NID:G199473; PIDN:AAA39626.1; PID:G199474
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:35-113/Domain: immunoglobulin homology <IMM>

Query Match 90.6%; Score 87; DB 2; Length 134;
 Best Local Similarity 81.2%; Pred. No. 6.6e-07;
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKPISGNSLFMYRQT 16
 |||||
 DB 42 CEPVSGHNDLFMYRQT 57

RESULT 6

S03488
 T-cell receptor beta chain precursor V region (clone HBP41) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 30-May-1997
 C:Accession: S03488
 R:Kimura, N.; Toyonaga, B.; Yoshikai, Y.; Triebel, F.; Debre, P.; Minden, M.D.; Mak, T.W.
 J. Exp. Med. 164, 739-750, 1986
 A>Title: Sequences and diversity of human T cell receptor beta chain variable region ge
 A:Reference number: S03485; MUID:86306525; PMID:3755748
 A:Accession: S03488

A:Molecule type: mRNA
 A:Residues: 1-93 <KIM>
 A:Cross-references: EMBL:X04925
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: T-cell receptor

Query Match 88.5%; Score 85; DB 2; Length 93;
 Best Local Similarity 87.5%; Pred. No. 9.8e-07;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKPISGNSLFMYRQT 16
 |||||
 DB 42 CKPISGHDLFMYRQT 57

RESULT 7

I38315
T-cell receptor beta chain V region (V-beta 8.2, germline) precursor - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jan-2000
C/Accession: I38315
R/SLightom, J.L.; Slemieniak, D.R.; Siew, L.C.; Koop, B.F.; Hood, L.
Genomics 20, 149-168, 1994
A/Title: Nucleotide sequence analysis of 77.7 kb of the human V beta T-cell receptor gene
A/Reference number: A54302; MUID:94292194; PMID:8020962
A/Accession: I38315
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-114 <RES>
A/Cross-references: EMBL:U03115; NID:g467918; PIDN:AAA17714.1; PID:g467924
C/Genetics: G2
A/Gene: TCRBV8S2
A/Intons: 17/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor
F/35-113/Domain: immunoglobulin homology <IMM>

Query Match 88.5%; Score 85; DB 2; Length 114;
Best Local Similarity 87.5%; Pred. No. 1.2e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKPISGHNSLFMYRQT 16
DB 42 CKPISGHDLFWYRQT 57

RESULT 8

S03511
T-cell receptor beta chain V region 8.2 precursor (clone H7.1 and others) - human
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
C/Accession: S03511; S78510; S78511; S26270; S26271
R/Siu, G.; Scirausa, E.C.; Lai, E.; Hood, L.E.
J. Exp. Med. 164, 1600-1614, 1986
A/Title: Analysis of a human V-beta gene subfamily.
A/Reference number: S03510; MUID:87035436; PMID:3772297
A/Accession: S03511
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-115 <STU>
A/Cross-references: EMBL:X07222
A/Experimental source: clone H7.1
A/Genetics: G1
A/Note: this sequence was determined from the germline gene
R/Plaza, A.
submitted to the EMBL Data Library, February 1991
A/Reference number: S78510
A/Accession: S78510
A/Molecule type: mRNA
A/Residues: 1-114 <PLA>
A/Cross-references: EMBL:X57619; NID:g23934; PIDN:CAA40845.1; PID:g23935
A/Experimental source: clone HT2.12
A/Genetics: G2
A/Accession: S78511
A/Molecule type: mRNA
A/Residues: 1, 'D', '3-114 <PLZ>
A/Cross-references: EMBL:X57720; NID:g23936; PIDN:CAA40887.1; PID:g23937
A/Experimental source: clone HT242
A/Genetics: G3
R/Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.
J. Immunol. 147, 4360-4365, 1991
A/Title: New human V-beta genes and polymorphic variants.
A/Reference number: S26255; MUID:92091749; PMID:1684376
A/Accession: S26270
A/Molecule type: mRNA
A/Residues: 1-96, 'R', '98-114 <PLM>
A/Cross-references: EMBL:X57619

A/Experimental source: clone HT2.12

A/Genetics: G2
A/Note: the authors translated the codon GGC for residue 2 as Asp
A/Accession: S26271
A/Molecule type: mRNA
A/Residues: 1, 'D', '3-96, 'R', '98-114 <PLF>
A/Cross-references: EMBL:X57720
A/Experimental source: clone HT242
A/Genetics: G3
C/Genetics: <G1>
A/Gene: 8.2
A/Intons: 17/1
A/Genetics: <G2>
A/Genetics: <G2>
A/Genetics: <G3>
A/Gene: 8.2b
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor
F/1-21/Domain: signal sequence #status predicted <SIG>
F/12-115/Product: T-cell receptor beta chain (fragment) #status predicted <MAT>
F/12-115/Domain: V region (V-beta 8.2) #status predicted <VRE>
F/35-113/Domain: immunoglobulin homology <IMM>

Query Match 88.5%; Score 85; DB 2; Length 115;
Best Local Similarity 87.5%; Pred. No. 1.2e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKPISGHNSLFMYRQT 16
DB 42 CKPISGHDLFWYRQT 57

RESULT 9

S57870
T cell receptor CK10 beta chain - human
C/Species: Homo sapiens (man)
C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C/Accession: S57870
R/Giegerich, G.; Petre, M.; Mehl, E.; Epplen, J.T.; Wekerle, H.; Hinkkanen, A.
Eur. J. Immunol. 22, 753-758, 1992
A/Title: Diversity of T cell receptor alpha and beta chain genes expressed by human T ce
A/Reference number: S57869; MUID:92192091; PMID:1372258
A/Accession: S57870
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-133 <GIB>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor
F/35-113/Domain: immunoglobulin homology <IMM>

Query Match 88.5%; Score 85; DB 2; Length 133;
Best Local Similarity 87.5%; Pred. No. 1.4e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKPISGHNSLFMYRQT 16
DB 42 CKPISGHNSDYMYRQT 57

RESULT 10

A27553
T-cell receptor beta chain precursor V region (VAK) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C/Accession: A27553
R/Epplen, J.T.; Bartels, F.; Becker, A.; Netz, G.; Prester, M.; Rinaldy, A.; Simon, M.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 4441-4445, 1986
A/Title: Change in antigen specificity of cytotoxic T lymphocytes is associated with the
A/Reference number: A27553; MUID:86233444; PMID:3487087
A/Accession: A27553
A/Molecule type: DNA
A/Residues: 1-114 <EBP>
A/Cross-references: GB:L29434; GB:M12775; GB:N00046; NID:g459887; PIDN:AAA40218.1; PID:g

A>Note: this sequence was determined from the germline gene
C:Comment: See entry PIR:A02002.

A:introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-114/Product: T-cell receptor beta chain V region VAK #status predicted <VAR>
F:35-113/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 81; DB 2; Length 114;
Best Local Similarity 75.0%; Pred. No. 5.3e-06;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYROT 16
DB 42 CEPISGSAVFWYROT 57

RESULT 11

RMSB3
T-cell receptor beta chain precursor V region (CTL-F3) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 30-May-1997
C:Accession: A02002
R:Chou, H.S.; Behlke, M.A.; Godambe, S.A.; Russell, J.H.; Brooks, C.G.; Ioh, D.Y.
EMBO J. 5, 2149-2155, 1986

A:Title: T cell receptor genes in an alleloreactive CTL clone: implications for rearrangement
A:Reference number: A91048; MUID:87053852; PMID:3490968
A:Accession: A02002

A:Molecule type: mRNA
A:Residues: 1-134 <CHO>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein; heterotrimer; T-cell receptor
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-114/Product: T-cell receptor beta chain precursor V region (CTL-F3) #status predicted
F:20-113/Region: V segment
F:35-113/Domain: immunoglobulin homology <IMM>
F:16-119/Region: D segment
F:120-134/Region: J segment
F:42-111/Distalide bonds: #status predicted
F:90/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 84.4%; Score 81; DB 1; Length 134;
Best Local Similarity 75.0%; Pred. No. 6.3e-06;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYROT 16
DB 42 CEPISGSAVFWYROT 57

RESULT 12

S21651
T-cell receptor beta chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S21651
R:Yanagishi, H.
Submitted to the EMBL Data Library, November 1990
A:Reference number: S21643

A:Accession: S21651
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-145 <YAM>
A:Cross-references: EMBL:X56708; NID:954647; PIDN:CAA40038.1; PID:954648
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F:35-113/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 81; DB 2; Length 145;
Best Local Similarity 75.0%; Pred. No. 6.8e-06;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYROT 16
DB 42 CEPISGSAVFWYROT 57

RESULT 13

RMSB3C
T-cell receptor beta chain precursor (F5) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-Aug-1984 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C:Accession: S03715; S25118; A02134; A9336; B9333
R:Palmer, M.S.; Bentley, A.; Gould, K.; Townsend, A.R.M.
Nucleic Acids Res. 17, 2353, 1989
A:Title: The T cell receptor from an influenza-A specific murine CTL clone.
A:Reference number: S03715; MUID:89202046; PMID:2784852
A:Accession: S03716

A:Molecule type: mRNA
A:Residues: 1-307 <PAL>
A:Cross-references: EMBL:X14388; NID:954668; PIDN:CAA32563.1; PID:954669
R:Austrop, F.; Kodella, V.; Kucharzik, T.; Kisch, E.
submitted to the EMBL Data Library, July 1992
A:Description: Characterization of idiotypic-specific I-Ed-restricted T suppressor lymphocyte mice.

A:Reference number: S25117
A:Accession: S25118
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-'GICR', 6,'C',8,'VFYV',14,'I',16,'NH',19,'D',21-23,'T',25-29,'E',31,'AE',
'K',86,'E',88,'L',90,'S',92,'F',94-99,'P',101,'E',103,'K',105-114,'IDNSAE',117,125-126
A:Cross-references: EMBL:X67128; NID:954678; PIDN:CAA47607.1; PID:954679
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotrimer; receptor; T-cell; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-307/Product: T-cell receptor beta chain #status predicted <VAR>
F:158-228/Domain: immunoglobulin homology <IMM>
F:281-302/Domain: transmembrane #status predicted <IMM>
F:303-307/Domain: intracellular #status predicted <INT>

Query Match 84.4%; Score 81; DB 1; Length 307;
Best Local Similarity 75.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYROT 16
DB 42 CEPISGSAVFWYROT 57

RESULT 14

S17379
T-cell receptor beta chain V region (clone IGRB02) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17379
R:Ferradini, L.; Roman-Roman, S.; Accor, J.; Michalaki, H.; Triebel, F.; Hercend, T.
Eur. J. Immunol. 21, 935-942, 1991
A:Title: Studies on the human T cell receptor alpha/beta variable region genes. II. Ide
A:Reference number: S17379; MUID:91209402; PMID:1826889
A:Accession: S17379

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-114 <FER>
A:Cross-references: EMBL:X58797; NID:933527; PIDN:CAA41603.1; PID:933528
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F:36-113/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 80; DB 2; Length 114;
Best Local Similarity 80.0%; Pred. No. 7.8e-06;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYROT 15
DB 42 CEPISGSAVFWYROT 57

DB 42 CNPISGHNTLYWYRQ 56

RESULT 15

I38316
T-cell receptor beta chain V region (V-beta 8.3, germline) precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jan-2000
C:Accession: I38316
R:Sliptron, J.L.; Siemieniak, D.R.; Sieu, L.C.; Koop, B.F.; Hood, L.
Genomics 20, 149-168, 1994
A:Title: Nucleotide sequence analysis of 77.7 kb of the human V beta T-cell receptor gen
A:Reference number: A54302; XUID:94292194; PMID:8020962
A:Accession: I38316
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-114 <RES>
A:Cross-references: EMBL:U03115; NID:9467918; PID:AAA17715.1; PID:9467925
C:Gene: TCRBV83
A:Gene: TCRBV83
A:introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F:35-113/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 80; DB 2; Length 114;
Best Local Similarity 75.0%; Pred. No. 7.8e-06;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKPIGHNLSFWYROT 16
DB 42 CQPIGHNTVFWYROT 57

Search completed: March 5, 2004, 16:36:49
Job time : 31 secs


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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_Taxid=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=87051852; PubMed=3490968;
RA Chou H.S., Behlke M.A., Godambe S.A., Russell J.H., Brooks C.G.,
  Loh D.Y.;
RT "T cell receptor genes in an allelically diverse CTL clone: implications for
  rearrangement and germ-line diversity of variable gene segments";
RL EMO J. 5:219-235(1986).
DR PIR; A02002; RMM5B3.
DR HSSP; P80748; 2L01.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_1.
DR SMART; SM00409; IG_1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW T-cell; Receptor; Immunoglobulin domain; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 134
FT FT T-CELL RECEPTOR BETA CHAIN V REGION CTL-
FT FT F3.
FT DOMAIN 20 115 V SEGMENT.
FT DOMAIN 116 119 D SEGMENT.
FT DOMAIN 120 134 J SEGMENT.
FT DISULFID 42 111 BY SIMILARITY.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. .) (POTENTIAL).
FT NON TER 134 134
SQ SEQUENCE 134 AA; 14946 MW; C080FB24C81988F6 CRC64;

Query Match 84.4%; Score 81; DB 1; Length 134;
Best Local Similarity 75.0%; Pred. No. 1.1e-06;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKPISGNSLFVYROT 16
Db 42 CDPISGSHAVFYROT 57
|:|||||:|||||
|:|||||:|||||

RESULT 3
TVE2_HUMAN STANDARD; PRT; 133 AA.
ID TVE2_HUMAN
AC P04435;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell receptor beta chain V region CTL-L17 precursor.
GN TCRB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
CX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=86276770; PubMed=2426193;
RA Leiden J.M., Frazer J.D., Strominger J.L.;
RT "The complete primary structure of the T-cell receptor genes from an
  allelically diverse human T-lymphocyte clone";
RL Immunogenetics 24:17-23(1986).
CC -I- MISCELLANEOUS: This sequence was derived from a human cytotoxic
  T-lymphocyte that is T3+, T4+, T8-.
CC -----
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CC -----
DR EMBL; M15564; AAA61027.1; -.
DR PIR; A02001; RMM7B.
DR HSSP; P01607; IREI.
```

```
DR Genew; HGNC:12155; TRB6.
DR GO; GO:0005886; C:Plasma membrane; NAS.
DR GO; GO:0003723; F:defense/immunity protein activity; NAS.
DR GO; GO:0042287; F:MHC protein binding; NAS.
DR GO; GO:0042605; F:peptide antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.
DR Pfam; PF00047; IG_1.
DR SMART; SM00409; IG_1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW T-cell; Receptor; Immunoglobulin domain; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 133
FT FT T-CELL RECEPTOR BETA CHAIN V REGION CTL-
FT FT L17.
FT DOMAIN 22 114 V SEGMENT.
FT DOMAIN 115 118 D SEGMENT.
FT DOMAIN 119 133 J SEGMENT.
FT CARBOHYD 30 30 N-LINKED (GLCNAC. .).
FT DISULFID 42 111 N-LINKED (GLCNAC. .).
FT NON TER 133 133
SQ SEQUENCE 133 AA; 14999 MW; 21030818D18D341F CRC64;

Query Match 77.1%; Score 74; DB 1; Length 133;
Best Local Similarity 75.0%; Pred. No. 1.6e-05;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CKPISGNSLFVYROT 16
Db 42 CDPISGSHAVFYROT 57
|:|||||:|||||
|:|||||:|||||

RESULT 4
TCE_FLV STANDARD; PRT; 321 AA.
ID TCE_FLV
AC P11364;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell receptor beta chain T17T-22 precursor.
GN V-TCR.
OS Feline leukemia virus.
OC Viruses; Retroviral viruses; Retroviridae; Gammaretrovirus.
CX NCBI_Taxid=11768;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=87144638; PubMed=3029597;
RA Fulton R., Forrest D., McFarlane R., Onions D., Neil J.C.;
RT "Retroviral transduction of T-cell antigen receptor beta-chain and
  myc genes";
RL Nature 326:190-194(1987).
RN (12)
RP REVISION TO 158-159.
RA Fulton R.;
RL Submitted (DEC-1987) to the EMBL/GenBank/DBJ databases.
CC -----
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  or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X05155; CAA28801.1; -.
DR PIR; C26600; RMMVTC.
DR HSSP; P01703; 7EAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR Pfam; PF00047; IG1_2.
DR SMART; SM00407; IG1_1.
DR PROSITE; PS50835; IG-LIKE; 2.
```

```

KW T-cell; Receptor; Immunoglobulin domain; Glycoprotein; Signal.
FT SIGNAL 1 28
FT CHAIN 29 321 T-CELL RECEPTOR BETA CHAIN T17T-22.
FT DOMAIN 29 132 V SEGMENT.
FT DOMAIN 123 128 D SEGMENT.
FT DOMAIN 129 145 U SEGMENT.
FT DOMAIN 321 145 C REGION.
SQ SEQUENCE 321 AA; 35581 MW; 11D2C3BF5681129 CRC64;

Query Match
Best Local Similarity 73.3%; Score 67; DB 1; Length 321;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CKPISGNSLFWYRQ 15
Db 51 CFPISGHSLSLYWYQ 65

RESULT 5
TVB8_MOUSE STANDARD; PRT; 130 AA.
AC P06321;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell receptor beta chain V region A20.2.25 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86068062; PubMed=3906657;
RA Morinaga T., Fotedar A., Singh B., Wegmann T.G., Tamacki T.;
RT "Isolation of cDNA clones encoding a T-cell receptor beta-chain from
a beef insulin-specific hydridoma."
RL Proc. Natl. Acad. Sci. U.S.A. 82:8163-8167(1985).
DR PIR; A02005; RWS20.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; IG_1.
DR SMART; SM00409; IG_1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR T-cell; Receptor; Immunoglobulin domain; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 >130 T-CELL RECEPTOR BETA CHAIN V REGION
FT DOMAIN 22 112 A20.2.25.
FT DOMAIN 113 115 V SEGMENT.
FT DOMAIN 116 130 D SEGMENT.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 14732 MW; 6721EC70DC64BEDB CRC64;

Query Match
Best Local Similarity 58.3%; Score 56; DB 1; Length 130;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CKPISGNSLFWYRQ 16
Db 41 CQGHGHNMYWYKQS 56

RESULT 6
TVB2_MOUSE STANDARD; PRT; 133 AA.
AC P01735;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell receptor beta chain V region 86T1 precursor.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c;
RX MEDLINE=84142271; PubMed=6546606;
RA Hedrick S.M., Nielsen E.A., Kavalier J., Cohen D.I., Davis M.M.;
RT "Sequence relationships between putative T-cell receptor polypeptides
and Immunoglobulins."
RL Nature 308:153-158(1984).
DR PIR; A02004; RWS28.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; IG_1.
DR SMART; SM00409; IG_1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW T-cell; Receptor; Immunoglobulin domain; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 133 T-CELL RECEPTOR BETA CHAIN V REGION 86T1.
FT DOMAIN 22 113 V SEGMENT.
FT DOMAIN 114 133 J SEGMENT.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .)
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .)
FT DISULFID 41 109 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14986 MW; 73EB9BEF6F85290 CRC64;

Query Match
Best Local Similarity 58.3%; Score 56; DB 1; Length 133;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CKPISGNSLFWYRQ 16
Db 41 CQGHGHNMYWYKQS 56

RESULT 7
TVB1_MOUSE STANDARD; PRT; 135 AA.
AC P01734;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell receptor beta chain V region 3H.25 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85176939; PubMed=2580639;
RA Govezman J., Minard K., Shastri N., Hunkapiller T., Hansburg D.,
RA Sercarz E., Hood L., Shastri N., Hunkapiller T., Hansburg D.,
RT "Rearranged beta T cell receptor genes in a helper T cell clone
specific for lysozyme: no correlation between V beta and MHC
restriction."
RL Cell 40:859-867(1985).
CC -1- MISCELLANEOUS: This T-cell clone expresses only a single V-beta
chain segment although it has three rearrangements in the beta
chain family.
CC -1- MISCELLANEOUS: This rearranged v-beta chain segment, specific for
chicken egg-white lysozyme and I-A(b), is the same as that
expressed in a T helper cell specific for cytochrome C and an
I-E(X) MHC molecule.
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CC EMBL: M12415; AAA40249.1; -.
DR PIR: A02003; RMMSEV.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003599; Ig.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00409; Ig; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
KM T-cell; Receptor; Immunoglobulin domain; Signal.
FT SIGNAL 1 20
FT CHAIN 21 135 T-CELL RECEPTOR BETA CHAIN V REGION
FT 3H.25.
FT DOMAIN 21 115 V SEGMENT.
FT RN 116 118 D SEGMENT.
FT DOMAIN 119 135 J SEGMENT.
FT DISULFID 42 111 BY SIMILARITY.
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 15123 MW; CQFLDDACF37E76D CRC64;

```

```

Query Match 53.1%; Score 51; DB 1; Length 135;
Best Local Similarity 53.3%; Pred. No. 0.13;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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Qy 1 CKPISGNSLFWTRQ 15
Db 42 CIREKHPVFWYQQ 56

```

RESULT 8

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TVB5_MOUSE
ID TVB5_MOUSE STANDARD; PRT; 122 AA.
AC P04212;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell receptor beta chain V region C5 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX MEDLINE=85036636; PubMed=6092964;
RA Patten P., Yokota T., Rothbard J., Chien Y., Arai K., Davis M.M.;
RT "Structure, expression and divergence of T-cell receptor beta-chain
RT variable regions."
RL Nature 312:40-46(1994).
CC -1- MISCELLANEOUS: This sequence was derived from a T-helper clone.
CC PIR: A02008; RMMSCS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
KM T-cell; Receptor; Immunoglobulin domain; Signal.
FT NON_TER 1 1
FT SIGNAL <1 7
FT CHAIN 8 122 T-CELL RECEPTOR BETA CHAIN V REGION C5.
FT RN 103 108 V SEGMENT.
FT DOMAIN 104 108 D SEGMENT.
FT DOMAIN 109 122 J SEGMENT.
FT DISULFID 31 99 BY SIMILARITY.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13349 MW; D657DC9B261C64C CRC64;

```

```

Query Match 49.0%; Score 47; DB 1; Length 122;
Best Local Similarity 40.0%; Pred. No. 0.54;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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Qy 1 CKPISGNSLFWTRQ 15
Db 31 CQTNNDHDTWYMYRQ 45

```

RESULT 9

```

TVB4_MOUSE
ID TVB4_MOUSE STANDARD; PRT; 136 AA.
AC P04212;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell receptor beta chain V region LB2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX MEDLINE=85036636; PubMed=6092964;
RA Patten P., Yokota T., Rothbard J., Chien Y., Arai K., Davis M.M.;
RT "Structure, expression and divergence of T-cell receptor beta-chain
RT variable regions."
RL Nature 312:40-46(1994).
CC -1- MISCELLANEOUS: This sequence was derived from a T-helper clone.
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CC
CC DR EMBL: X01643; CAA25800.1; -.
CC PIR: A02007; RMMSLB.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003599; Ig.
CC Pfam: PF00047; Ig; 1.
CC SMART: SM00409; Ig; 1.
CC PROSITE: PSS0835; IG_LIKE; 1.
KM T-cell; Receptor; Immunoglobulin domain; Signal.
FT SIGNAL 1 21
FT CHAIN 22 136 T-CELL RECEPTOR BETA CHAIN V REGION LB2.
FT RN 117 120 V SEGMENT.
FT DOMAIN 121 136 D SEGMENT.
FT DOMAIN 121 136 J SEGMENT.
FT DISULFID 45 113 BY SIMILARITY.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15369 MW; F74DCC0414088D02 CRC64;

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Query Match 49.0%; Score 47; DB 1; Length 136;
Best Local Similarity 40.0%; Pred. No. 0.61;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 CKPISGNSLFWTRQ 15
Db 45 CQTNNDHDTWYMYRQ 59

```

RESULT 10

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Y137_ADE02
ID Y137_ADE02 STANDARD; PRT; 137 AA.
AC P03293;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE Hypothetical protein B-137.
OS Human adenovirus type 2.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515;
RN [1]
RX MEDLINE=83056643; PubMed=7142161;
RA Ginges T.R., Sclary D., Gelinas R.E., Bing-Dong J., Yen C.E.,
RA Kelly M.M., Bullock P.A., Parsons B.L., O'Neill K.E., Roberts R.J.;
RT "Nucleotide sequences from the adenovirus-2 genome."

```

RL J. Biol. Chem. 257:13475-13491(1982).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=83056844; PubMed=7142162;

RA Alestrom P., Akusjærvi G., Pettersson M., Pettersson U.;

RT "DNA sequence analysis of the region encoding the terminal protein

RT and the hypothetical N-gene product of adenovirus type 2.";

RL J. Biol. Chem. 257:13492-13498(1982).

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CC

CC EMBL; J01917; -; NOT_ANNOTATED_CDS.

DR PIR; E92351; A03865.

KW Hypothetical protein.

SC SEQUENCE 137 AA; 14366 MW; B7ACA61A63116856 CRC64;

Query Match 49.0%; Score 47; DB 1; Length 137;

Best Local Similarity 50.0%; Pred. No. 0.62;

Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 KPISGNSLFMY 13

Db 60 EPVSGHSSVYMW 71

RESULT 11

ID NU2M HANWI STANDARD; PRT; 567 AA.

AC P48906;

DT 01-FEB-1996 (Rel. 33, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).

GN ND2.

OS Hansenula winei (Yeast).

OC Mitochondrion.

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Pichia.

OX NCBI_Taxid=4907;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=21;

RA Sekito T., Okamoto K., Kitano H., Yoshida K.;

RT "Yeast Hansenula winei mitochondrial genome's complete DNA sequence

RT demonstrated unique characteristics.";

RT Nucleic Acids Symp. Ser. 31:235-234(1994).

CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial

CC inner membrane.

CC -1- SIMILARITY: Belongs to the complex I subunit 2 family.

CC

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CC

CC EMBL; D31785; BA06573.2; -

DR PIR; S58750; S58750.

DR InterPro; IPR001750; Oxidored_q1.

DR Pfam; PF00361; Oxidored_q1; 1.

KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.

SC SEQUENCE 567 AA; 65298 MW; 8BA748C3E26F290 CRC64;

Query Match 49.0%; Score 47; DB 1; Length 567;

Best Local Similarity 88.9%; Pred. No. 2.9;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 SGHNSLFMY 13

Db 184 SGHNSLFMY 192

RESULT 12

ID PH11 SYNY3 STANDARD; PRT; 748 AA.

AC Q55168;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Phytochrome-like protein cph1 (EC 2.7.3.-) (light-regulated histidine

DE kinase 1) (Bacteriophytochrome cph1).

GN CPH1 OR SLR0473.

OS Synechocystis sp. (strain PCC 6803).

OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.

OX NCBI_Taxid=1148;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96127529; PubMed=8590279;

RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,

RA Sugita M., Tabata S.;

RT "Sequence analysis of the genome of the unicellular cyanobacterium

RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb

RT region from map positions 648 to 928 of the genome.";

RL DNA Res. 2:153-166(1995).

RN [2]

RP CHARACTERIZATION, AND MUTAGENESIS OF HIS-260.

RX MEDLINE=97426627; PubMed=9278513;

RA Yeh K.-C., Wu S.-H., Murphy J.T., Lagarias J.C.;

RT "A cyanobacterial phytochrome two-component light sensory system.";

RL Science 277:1505-1508(1997).

RN [3]

RP CHARACTERIZATION.

RX MEDLINE=20290819; PubMed=10828948;

RA Park C.-M., Shim J.-Y., Yang S.-S., Kang J.-G., Kim J.-I., Luka Z.,

RA Song P.-S.;

RT "Chromophore-apoptoprotein interactions in Synechocystis sp. PCC6803

RT phytochrome Cph1.";

RL Biochemistry 39:6349-6356(2000).

CC -1- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT

CC ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT. THE R FORM THAT ABSORBS

CC MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE FR FORM THAT

CC ABSORBS MAXIMALLY IN THE FAR-RED REGION. HAS ALSO A SLIGHT BLUE

CC SHIFT FOR THE FAR-RED MAXIMUM. FORMS A TWO-COMPONENT SYSTEM WITH

CC THE RCP1 RESPONSE REGULATOR.

CC

CC -1- SUBUNIT: Homodimer.

CC

CC -1- PTM: Contains one covalently linked tetrahydropole chromophore (By

CC similarity).

CC -1- MISCELLANEOUS: THE R FORM EXHIBITS BOTH ATP-DEPENDENT

CC AUTOPHOSPHORYLATION AND PHOSPHOTRANSFER TO RCP1 ACTIVITIES. UNLIKE

CC THE HIGHER PLANTS WHERE PFR IS THOUGHT TO BE THE ACTIVE FORM.

CC

CC -1- SIMILARITY: In the N-terminal section, belongs to the phytochrome

CC family.

CC

CC -1- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.

CC

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CC

CC EMBL; D64001; BAA10307.1; -

DR PIR; S74389; S74389.

DR InterPro; IPR003594; ATPbind_ATPase.

DR InterPro; IPR004358; Bact_sens_pr_C.

```

DR InterPro: IPR003018; GAF.
DR InterPro: IPR003661; His_KinA_N.
DR InterPro: IPR005467; His_Kinase.
DR InterPro: IPR000014; PAS_Domain.
DR InterPro: IPR001294; Phytochrome.
DR Pfam: PF01590; GAF; 1.
DR Pfam: PF02518; HATPase_C; 1.
DR Pfam: PF00512; HisKA; 1.
DR Pfam: PF00360; phytochrome; 1.
DR PRINTS: PR00344; BCTRLSENSOR.
DR PRINTS: PR01033; PHYTOCHROME.
DR SMART: SM00065; GAF; 1.
DR SMART: SM00387; HATPase_C; 1.
DR SMART: SM00388; HisKA; 1.
DR SMART: SM00091; PAS; 1.
DR PROSITE: PS50109; HIS_KIN; 1.
DR PROSITE: PS50112; PAS; FALSE_NEG.
DR PROSITE: PS50245; PHYTOCHROME_1; FALSE_NEG.
DR PROSITE: PS50046; PHYTOCHROME_2; 1.
DR PROSITE: PS50046; Phytochrome; Kinase; Phosphorylation;
KW Sensory transduction; Transferase; Kinase; Complete proteome.
FT DOMAIN 19 86
FT BINDING 535 748 CHROMOPHORE BINDING DOMAIN.
FT BINDING 260 260 HISTIDINE KINASE.
FT MOD_RES 538 538 CHROMOPHORE (BY SIMILARITY).
FT MUTAGEN 538 538 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
H->K: NO AUTOPHOSPHORYLATION; NO
PHOSPHOTRANSFER TO RCPL.
SQ SEQUENCE 748 AA; 84232 MW; A9ECA6DBD5B3C88A CRC64;

Query Match 46.9%; Score 45; DB 1; Length 748;
Best Local Similarity 58.3%; Pred. No. 8.5;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PISCHNSLFWYR 14
DQ 430 PIAHNFILMR 441

RESULT 13
TVB3 MOUSE STANDARD; PRT; 120 AA.
ID TVB3 MOUSE
AC P01736;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell receptor beta chain V region PHDS203 precursor (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB B.
RA MEDLINE=84245824; PubMed=6330561; Hayday A.C., Eisen H.N.,
RA Saito H., Krantz D.M., Takagaki Y., Hayday A.C., Eisen H.N.,
RA Tonesgawa S.;
RT "Complete primary structure of a heterodimeric T-cell receptor
RT deduced from cDNA sequences."
RT Nature 309:757-762 (1984).
RL -1- MISCELLANEOUS: This clone was isolated from a cytotoxic T
CC lymphocyte.
CC PIR: A02006; RKM5V2.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003599; Ig.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00409; Ig; 1.
KW T-cell: Receptor; Immunoglobulin domain; Signal.
FT NON_TER 1 1
FT SIGNAL <1 11
FT CHAIN 12 120 T-CELL RECEPTOR BETA CHAIN V REGION
FT DOMAIN 12 106 PHDS203.
V SEGMENT.

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FT DOMAIN 107 120 J SEGMENT.
FT DISULFID 34 102 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13670 MW; DB1011504969DCE CRC64;

Query Match 45.8%; Score 44; DB 1; Length 120;
Best Local Similarity 40.0%; Pred. No. 1.7;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYRQ 15
DQ 34 CGQDWSHETWYWRQ 48

RESULT 14
RPMW ARCFU STANDARD; PRT; 103 AA.
ID RPMW ARCFU
AC O29033;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE DNA-directed RNA polymerase subunit M (EC 2.7.7.6).
GN RPMW OR AF1235.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Kleink H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickley E.K., Peterson J.D.,
RA Richardson D.L., Kervlavage A.R., Graham D.E., Kyriades N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirtress E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370 (1997).
DE -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
DE of DNA into RNA using the four ribonucleoside triphosphates as
DE substrates.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA) (N).
CC -1- SIMILARITY: Belongs to the archaeal rpmw / eukaryotic
CC RPA12/RPB9/RPC11 RNA polymerase family.
CC -1- SIMILARITY: Contains 1 ribbon-type zinc finger.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AE001019; AB900009.1; -
CC PIR: B69404; B69404.
CC HSSP: Q36254; 1QYF.
CC TIGR: AF1235; -
DR InterPro: IPR001529; RNA_p01M.
DR InterPro: IPR001222; TFIIS.
DR InterPro: IPR006288; Trans_facts.
DR Pfam: PF02150; RNA_POL_M_15KD; 1.
DR Pfam: PF01096; TFIIS; 1.
DR SMART: SM00661; RPB015; 1.
DR SMART: SM00440; ZNF_C2C2; 1.

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DR TIGRPM6; TIGR01384; TFS arch; 1.
 DR PROSITE; PS00466; TFRS_1
 DR PROSITE; PS01030; RNA_POL_M15KD; 1.
 KM Transferrase; DNA-directed RNA polymerase; Transcription; Zinc-finger;
 FT Complete proteome.
 FT ZN_FING 4 23 C4-TYPE.
 FT ZN_FING 64 95 ZN-RIBON.
 SQ SEQUENCE 103 AA; 12057 MW; 4C1B9F2AC1C1B62B CRC64;

Query Match 44.8%; Score 43; DB 1; Length 103;
 Best Local Similarity 54.5%; Pred. No. 2.1;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 PISGHSLSFWY 13
 DB 65 PACGHNEAFMW 75

RESULT 15
 ID VA43 VACCC STANDARD; PRT; 194 AA.
 AC P21065;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein A43.
 GN A43R.
 OS Vaccinia virus (strain Copenhagen).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10249;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91021027; PubMed=2219722;
 RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
 RA Paoletti E.;
 RT "The complete DNA sequence of vaccinia virus."
 RL Virology 179:247-266(1990).
 RN (2)
 RP COMPLETE GENOME.
 RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
 RA Paoletti E.;
 RT "Appendix to 'The complete DNA sequence of vaccinia virus'."
 RL Virology 179:517-563(1990).
 CC -----
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 CC -----
 CC EMBL; M35027; AAA48174.1; -
 DR PIR; I42521; I42521.
 SQ SEQUENCE 194 AA; 22635 MW; 639990229C05591F CRC64;

Query Match 43.8%; Score 42; DB 1; Length 194;
 Best Local Similarity 42.9%; Pred. No. 6.3;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 CKRPSGHSLSFWY 14
 DB 144 CIRIIGYDSIIWYK 157

Search completed: March 5, 2004, 16:35:18
 Job time : 16 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 5, 2004, 16:29:20 / Search time 39 Seconds

(without alignments)
129,443 Million cell updates/sec

Title: US-09-591-789-1

Perfect score: 96

Sequence: 1 CKPISGHSLEFWYROT 16

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	72.9	310	4 Q8N2T6	Q8N2T6 homo sapien
2	56	58.3	127	11 Q9D3G4	Q9D3G4 mus musculu
3	56	58.3	303	11 O7TND8	O7TND8 mus musculu
4	51	53.1	1157	10 O7XSH1	O7XSH1 cryza sativ
5	50	52.1	89	7 Q86DP8	Q86DP8 mus sp. cia
6	47	49.0	577	11 Q21XG6	Q21XG6 mus musculu
7	47	49.0	615	11 Q62687	Q62687 rattus norv
8	47	49.0	615	11 Q88576	Q88576 mus musculu
9	46	47.9	621	10 Q9FTF3	Q9FTF3 oryza sativ
10	46	47.9	257	16 Q89UM3	Q89UM3 bradyrhizob
11	45.5	47.4	326	17 Q8TNE4	Q8TNE4 methanococ
12	45	46.9	186	16 Q88J13	Q88J13 pseudomonas
13	45	46.9	269	17 Q97W63	Q97W63 sulfobac
14	45	46.9	421	10 Q9S190	Q9S190 arabidopsi
15	44	45.8	215	11 Q9D2W6	Q9D2W6 mus musculu
16	44	45.8	234	11 Q6R3W1	Q6R3W1 mus musculu

17	44	45.8	234	11 Q99N04	Q99N04 mus musculu
18	44	45.8	267	11 Q8BV59	Q8BV59 mus musculu
19	44	45.8	342	13 Q8AXL4	Q8AXL4 oncorhynch
20	44	45.8	428	16 Q9L2D5	Q9L2D5 streptomyce
21	44	45.8	566	10 Q9JPM2	Q9JPM2 arabidopsi
22	44	45.8	688	2 Q8VNX1	Q8VNX1 bacillus th
23	44	45.8	1104	11 Q8R4D5	Q8R4D5 mus musculu
24	44	45.8	1104	11 Q8R4D5	Q8R4D5 mus musculu
25	43	44.8	211	12 Q8JL77	Q8JL77 ectromelia
26	43	44.8	225	13 Q7ZT04	Q7ZT04 paracitochy
27	43	44.8	235	13 Q90770	Q90770 gallus gall
28	43	44.8	331	12 Q98337	Q98337 murine hepa
29	43	44.8	361	10 P94013	P94013 oryza sativ
30	43	44.8	443	16 Q8EY44	Q8EY44 leptospira
31	43	44.8	504	8 Q9GFE0	Q9GFE0 arabis lyr
32	43	44.8	504	8 Q9GFE42	Q9GFE42 arabis fend
33	43	44.8	504	8 Q9GFE48	Q9GFE48 arabis lign
34	43	44.8	504	8 Q9GFE46	Q9GFE46 halimolobos
35	43	44.8	504	8 Q9GFE38	Q9GFE38 crucihimala
36	43	44.8	504	8 Q9GFE44	Q9GFE44 arabis part
37	43	44.8	504	8 Q9GFE28	Q9GFE28 crucihimala
38	43	44.8	504	8 Q9GFE49	Q9GFE49 arabis drum
39	43	44.8	504	8 Q9GFE43	Q9GFE43 arabis drum
40	43	44.8	741	10 Q9FJ02	Q9FJ02 arabidopsi
41	43	44.8	1095	4 Q8TDX8	Q8TDX8 homo sapien
42	43	44.8	1104	4 Q8TDC3	Q8TDC3 homo sapien
43	43	44.8	1104	4 Q7Z2W7	Q7Z2W7 homo sapien
44	42.5	44.3	400	12 Q8B411	Q8B411 porcine lym
45	42.5	44.3	578	12 Q85314	Q85314 rabbit fibr

ALIGNMENTS

RESULT 1

Q8N2T6	PRELIMINARY;	PRT;	310 AA.
Q8N2T6	Q8N2T6		
AC	Q8N2T6		
DT	01-OCT-2002 (TIREMBLrel. 22, Created)		
DT	01-OCT-2002 (TIREMBLrel. 22, Last sequence update)		
DT	01-OCT-2003 (TIREMBLrel. 25, Last annotation update)		
DE	Hypothetical protein (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Blood;		
RA	Strauberg R.;		
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC030533; AA030533.1; -		
DR	InterPro: IPR003599; IG_1.		
DR	InterPro: IPR007110; IG_1-like.		
DR	InterPro: IPR003597; IG_1.		
DR	InterPro: IPR003596; IG_1.		
DR	Pfam; PF00047; IG_2.		
DR	SMART; SM00409; IG_1.		
DR	SMART; SM00407; IG_1.		
DR	SMART; SM00406; IG_1.		
DR	PROSITE; PSS0835; IG_1-like; 2.		
KM	Hypothetical protein.		
FT	NOM_TIR		
SQ	SEQUENCE 310 AA; 34431 MW; 828579E16A781D4B CRC64;		
Query Match	72.9%; Score 70; DB 4; Length 310;		
Best Local Similarity	68.8%; Pred. No. 0.0017;		
Matches	11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;		
QY	1 CKPISGHSLEFWYROT 16		
DB	41 CKPISGHSLEFWYROT 56		

Db 891 PSTGNSLFWYRQT 904

RESULT 5

0860P8 PRELIMINARY; PRT; 89 AA.
 ID 0860P8
 AC 0860P8
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Class II major histocompatibility complex I-A beta q chain beta 1 domain (Fragment).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10095;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94194182; PubMed=8144978;
 RA Orman R.A., Holderbaum D., Qu X.M., Banerjee S., Haqqi T.M.,
 RT "B2B/B2U (H-q) is a TCR deletion mutant mouse strain (TCR V beta a, XJ6-) that is susceptible to type II collagen-induced arthritis.";
 RL J. Immunol. 152:4175-4182(1994).
 DR EMBL; S69290; AAP19624.1; -
 DR InterPro; IPR007110; Ig-like.
 FT NON_TER 1
 FT NON_TER 89
 SQ SEQUENCE 89 AA; 10465 MW; B91673B5DFC28C3 CRC64;

Query Match 52.1%; Score 50; DB 7; Length 89;
 Best Local Similarity 40.0%; Pred. No. 1.1;
 Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CKPISGNSLFWYRQT 15
 Db 27 CEQTLIDHNTWYRQT 41

RESULT 6

091XG6 PRELIMINARY; PRT; 577 AA.
 ID 091XG6
 AC 091XG6
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Similar to X transporter protein 2.
 GN XTRP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RA Straussberg R.;
 RC TISSUE=Kidney;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBS databases.
 DR EMBL; BC010748; AAH10748.1; -
 DR WGD; MGI:1336892; Xtrp2.
 DR GO; GO:0005887; C:integral to plasma membrane; IEA.
 DR GO; GO:0005328; F:neurotransmitter:sodium symporter activity; IEA.
 DR GO; GO:0006836; P:neurotransmitter transporter; IEA.
 DR InterPro; IPR000175; Na/ntraan_symport.
 DR Pfam; PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR PRODOM; PD000448; Na/ntraan_symport; 2.
 DR PROSITE; PS50267; NA_NEUOTRAN_SYMP 3; 1.
 SQ SEQUENCE 577 AA; 65254 MW; 5F84F7G5CF1B1E3 CRC64;

Query Match 49.0%; Score 47; DB 11; Length 577;
 Best Local Similarity 75.0%; Pred. No. 22;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 SGHNSLFWYRQT 16

Db 154 SGTYSYFWYRQT 165

RESULT 7

062687 PRELIMINARY; PRT; 615 AA.
 ID 062687
 AC 062687
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Renal osmotic stress-induced Na-Cl organic solute cotransporter.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=SPRAGUE-DAWLEY; TISSUE=Kidney cortex;
 RX MEDLINE=95029937; PubMed=7943364;
 RA Wasserman J.C., Delplire E., Tonidandel W., Kojima R., Guillans S.R.;
 RT "Molecular characterization of ROSIT, a renal osmotic stress-induced Na(+) -Cl(-) -organic solute cotransporter.";
 RL Am. J. Physiol. 267:F688-F694(1994).
 DR EMBL; U12973; AAC13771.1; -
 DR GO; GO:0005887; C:integral to plasma membrane; IEA.
 DR GO; GO:0016020; F:membrane; IEA.
 DR GO; GO:0005328; F:neurotransmitter:sodium symporter activity; IEA.
 DR GO; GO:0006836; P:neurotransmitter transporter; IEA.
 DR InterPro; IPR000175; Na/ntraan_symport.
 DR Pfam; PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR PRODOM; PD000448; Na/ntraan_symport; 2.
 DR PROSITE; PS50267; NA_NEUOTRAN_SYMP 3; 1.
 SQ SEQUENCE 615 AA; 69556 MW; F41E7DEIDC276918 CRC64;

Query Match 49.0%; Score 47; DB 11; Length 615;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 SGHNSLFWYRQT 16
 Db 154 SGTYSYFWYRQT 165

RESULT 8

088576 PRELIMINARY; PRT; 615 AA.
 ID 088576
 AC 088576; 088577; 088578; 088580; 088581;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Sodium- and chloride-dependent transporter XTRP2.
 GN XTRP2 OR XT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
 RC TISSUE=KIDNEY;
 RX MEDLINE=99131080; PubMed=9932288;
 RX Naeh S.R., Gires B., Kingmore S.F., Kim K.M., El-Mestkawy S.,
 RA Dong Q., Fumagalli F., Seidlin M.F., Caron M.G.;
 RT "Cloning, gene structure, and genomic localization of an orphan transporter from mouse kidney with six alternatively-spliced isoforms.";
 RL Recept. Channels 6:113-128(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=6;
 CC Name=A12;
 CC IsoId=088576-1; Sequence=Displayed;

```

CC      Name=A11;
CC      IsoId=088576-2; Sequence=VSP_050365;
CC      Name=B11;
CC      IsoId=088576-3; Sequence=VSP_050364;
CC      Name=A10;
CC      IsoId=088576-4; Sequence=VSP_050366, VSP_050367;
CC      Name=B9;
CC      IsoId=088576-5; Sequence=VSP_050364, VSP_050366;
CC      Name=A8;
CC      IsoId=088576-6; Sequence=VSP_050363;
CC      -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN KIDNEY.
CC      -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
CC      FAMILY (SNF).
DR      EMBL: AF075262; AAC27757.1; -
DR      EMBL: AF075263; AAC27758.1; -
DR      EMBL: AF075264; AAC27759.1; -
DR      EMBL: AF075265; AAC27760.1; -
DR      EMBL: AF075266; AAC27761.1; -
DR      EMBL: AF075267; AAC27762.1; -
DR      MGI: MGI:1336892; Xlrp2.
DR      GO: GO:0005887; C: integral to plasma membrane; IEA.
DR      GO: GO:0005528; F: neurotransmitter: sodium symporter activity; IEA.
DR      GO: GO:0015593; F: symporter activity; IEA.
DR      InterPro: IPR00175; Na/ntrn_symport.
DR      Pfam: PF00209; SNF. 1.
DR      PRINTS: PR00176; NANEUSMPORT.
DR      ProDom: PD000448; Na/ntrn_symport; 2.
DR      PROSITE: PS00610; NA_NEUROTRAN_SYM_1; FALSE_NEG.
DR      PROSITE: PS00754; NA_NEUROTRAN_SYM_2; FALSE_NEG.
DR      PROSITE: PS50267; NA_NEUROTRAN_SYM_3; 1.
KW      Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
KW      Symport; Alternative splicing.
FT      DOMAIN 1 26
FT      TRANSMEM 27 47
FT      DOMAIN 48 52
FT      TRANSMEM 53 73
FT      DOMAIN 74 83
FT      TRANSMEM 84 104
FT      DOMAIN 105 105
FT      TRANSMEM 106 126
FT      DOMAIN 127 177
FT      TRANSMEM 178 198
FT      DOMAIN 199 206
FT      TRANSMEM 207 227
FT      DOMAIN 228 288
FT      TRANSMEM 289 309
FT      DOMAIN 310 397
FT      TRANSMEM 398 418
FT      DOMAIN 419 441
FT      TRANSMEM 442 462
FT      DOMAIN 463 472
FT      TRANSMEM 473 493
FT      DOMAIN 494 520
FT      TRANSMEM 521 541
FT      DOMAIN 542 570
FT      TRANSMEM 571 591
FT      DOMAIN 592 615
FT      CARBOHYD 353
FT      VARSPLIC 377 422
FT      VARSPLIC 377 444
FT      VARSPLIC 445 454
FT      VARSPLIC 499 552

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FT      Isoform A10 and isoform B9.
FT      /FtId=VSP_050366
FT      VARSPLIC 553 615 Missing (in isoform A10).
FT      /FtId=VSP_050367
SQ      SEQUENCE 615 AA; 69228 MW; A7925C0397FC63FB CRC64;
Query Match
Best Local Similarity 49.0%; Score 47; DB 11; Length 615;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      5 SGHSLFFMYRQT 16
DB      154 SGTVSYFWYRQT 165

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RESULT 9

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O9FTR3 PRELIMINARY; PRT; 621 AA.
AC      O9FTR3.
DT      01-MAR-2001 (TRENDELREL. 16, Created)
DT      01-OCT-2003 (TRENDELREL. 25, Last sequence update)
DE      Putative receptor kinase.
GN      P0463F06.16 OR OJ1212_B09.24.
OS      Oryza sativa (Rice)
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OX      Euphorbiaceae; Oryzae; Oryza.
NCBI_TaxID=4530;
[1]
RP      SEQUENCE FROM N.A.
RP      STRAIN=cv. Nipponbare;
RA      Saeki T., Matsumoto T., Yamamoto K.;
RT      "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT      clone:p0463f06."
RT      Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP      SEQUENCE FROM N.A.
RP      STRAIN=cv. Nipponbare;
RA      Saeki T., Matsumoto T., Yamamoto K.;
RT      "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC
RT      clone:OJ1212_B09."
RT      Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR      EMBL: AP002867; BAB17126.1; -
DR      EMBL: AP003338; BAB39451.1; -
DR      Gramene; O9FTR3; -
DR      GO: GO:0005524; F: ATP binding; IEA.
DR      GO: GO:0004674; F: protein serine/threonine kinase activity; IEA.
DR      GO: GO:0004872; F: receptor activity; IEA.
DR      GO: GO:0016740; F: transferase activity; IEA.
DR      GO: GO:0006468; P: protein amino acid phosphorylation; IEA.
DR      InterPro: IPR001092; HLH basic.
DR      InterPro: IPR000719; ProC_kinase.
DR      InterPro: IPR008271; Ser_thr_pkin_AS.
DR      Pfam: PF00069; Pkinase; 1.
DR      ProDom: PD000001; ProC_kinase; 1.
DR      PROSITE: PS00038; HLH_1; 1.
DR      PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR      PROSITE: PS50011; PROTEIN KINASE DOM; 1.
DR      PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW      ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW      Transferase.
SQ      SEQUENCE 621 AA; 69776 MW; 8D241127786B99EF CRC64;

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Query Match
Best Local Similarity 49.0%; Score 47; DB 10; Length 621;
Matches 9; Conservative 1; Mismatches 1; Indels 2; Gaps 1;
QY      3 PIS--GNSLFWY 13
DB      153 PISLGHNNQFWY 165

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RESULT 10
Q89UM3 PRELIMINARY; PRT; 257 AA.
ID Q89UM3
AC Q89UM3;
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
GN 1-acylglycerol-3-phosphate O-acyltransferase (EC 2.3.1.51).
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobiaceae.
NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=2248498; PubMed=12597275;
RA Kaneko T., Nakamura Y., Saito S., Minamisawa K., Uchiyama T.,
RA Sasamoto S., Matsunobe A., Idegawa K., Iritaguchi M., Kawashima K.,
RA Kohara M., Matsunobe M., Shimpo S., Isumoto H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
DR EMBL: AP005940; BAC4658.1;
DR GO: GO:0003841; F.1-acylglycerol-3-phosphate O-acyltransferase. . . ; IEA.
DR GO: GO:0008415; P.acyltransferase activity; IEA.
DR GO: GO:0016740; P.acyltransferase activity; IEA.
DR GO: GO:0008152; P.acyltransferase activity; IEA.
DR InterPro: IPR002123; Acyltransferase.
DR InterPro: IPR002129; RhodGEP.
DR Pfam: PF01553; Acyltransferase; Complete proteome.
DR KEGG: K01553; Acyltransferase; Complete proteome.
SQ SEQUENCE 257 AA; 28789 MW; 3C1BA53D5DA0A268 CRC64;

Query Match 47.9%; Score 46; DB 16; Length 257;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 CKPISGNSLFWYROT 16
Db 179 CLPILNSGLFMPRT 194

RESULT 11
Q8TNE4 PRELIMINARY; PRT; 326 AA.
ID Q8TNE4
AC Q8TNE4;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
GN Predicted protein.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=1193238;
RA Fitzgerald W., Nussbaum C., Roy A., Endrizzi M.G., MacDonald P.,
RA Allen N., Naylor J., Stange-Thomann N., Deatellano K., Johnson R.,
RA Linman L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Graham D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,
RA Perry J.G., Jarrell K.F., Ding H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;

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RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity."
RL Genome Res. 12:532-542(2002).
DR EMBL: AF010922; AAM05734.1;
KM Complete proteome.
SQ SEQUENCE 326 AA; 38705 MW; C006A0894B2B7A1 CRC64;

Query Match 47.4%; Score 45.5; DB 17; Length 326;
Best Local Similarity 69.2%; Pred. No. 22;
Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 CKPISGNSLFWY 13
Db 122 CKYVSG-RSLFWY 133

RESULT 12
Q88UJ3 PRELIMINARY; PRT; 186 AA.
ID Q88UJ3
AC Q88UJ3;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
GN Hypothetical protein.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=2423060; PubMed=12534463;
RA Nelson K.B., Knebel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beaman M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A.,
RA Ueberlack T., Rizzo M., Lee K., Kosack D., Moresl D., Medler H.,
RA Laubert J., Stjepanovic D., Hohnselt J., Straetz M., Helm S.,
RA Kewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuenmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL: AE016784; AAN68274.1;
DR TIGR: PP2666;
DR InterPro: IPR001763; Rhodanese-like.
DR PROSITE: PS50206; RHODANES_3;
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 186 AA; 20938 MW; DC7BC818EDBA2147 CRC64;

Query Match 46.9%; Score 45; DB 16; Length 186;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNSLFWYR 14
Db 156 GYNNILWYR 164

RESULT 13
Q9TWG3 PRELIMINARY; PRT; 269 AA.
ID Q9TWG3
AC Q9TWG3;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Hypothetical protein SSO2257.
GN SSO2257.
OS Sulfobacillus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfobacterales; Sulfobacterales;
OC Sulfobacillus.
NCBI_TaxID=2287;

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RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=21332286; PubMed=11427726;
 RA She Q., Singh R.K., Contaloni F., Zivanovic Y., Allard G.,
 RA Aayaz M.J., Chan-Welner C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moers A., Erasmo G., Fletcher C., Gordon P.M.K.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doollittle W.F., Duquet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Sengen C.W., Van der Oost J.,
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 DR EMBL; A6006830; AAK42424.1; -.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 269 AA; 30912 MW; 490B957E34230AD CRC64;

Query Match 46.9%; Score 45; DB 17; Length 269;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

Qy 2 KPISGNSLFMY 13
 Db 37 KPISGNSLFMY 46

RESULT 14
 Q9SY90 PRELIMINARY; PRT; 421 AA.
 AC Q9SY90;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE T25B24.5 protein.
 GN T25B24.5.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=5702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
 RA Altieri H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
 RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
 RA Lueros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
 RA Walker M., Yu G., Becker U., Theologis A., Davis R.W.,
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC005850; AAD25550.1; -.
 DR PIR; D96641; D96641.
 SQ SEQUENCE 421 AA; 48772 MW; 5B1ADF700118431E CRC64;

Query Match 46.9%; Score 45; DB 10; Length 421;
 Best Local Similarity 60.0%; Pred. No. 34;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GHNSLFMYRQ 15
 Db 301 GHGSPVYRQ 310

RESULT 15
 Q9D2W6 PRELIMINARY; PRT; 215 AA.
 AC Q9D2W6;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 913042210Rik protein.
 GN MS447 OR 913042210Rik.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arkawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuenli P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirni L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guelinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons F., Marchionni L., Mashima U., Mazzarelli U., Mombarto P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 DR EMBL; AK018686; BAB1344.1; -.
 DR MGD; MGI:1918846; Ms4a7.
 DR InterPro; IPR007237; CD20.
 DR Pfam; PF04103; CD20; 1.
 SQ SEQUENCE 215 AA; 23722 MW; 3C6B3C964E18ED3E CRC64;

Query Match 45.8%; Score 44; DB 11; Length 215;
 Best Local Similarity 41.7%; Pred. No. 26;
 Matches 5; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ISGNSLFMYRQ 15
 Db 176 LAGSSTLFMYRQ 187

Search completed: March 5, 2004, 16:36:09
 Job time : 43 secs